

(2) INFORMATION FOR SEQ ID NO: 1:

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TGCTTTAGCA ACAGCCTATC AG

22

(2) INFORMATION FOR SEQ ID NO: 2:

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TAAACTTCTT CCGGCACTTC G

21

(2) INFORMATION FOR SEQ ID NO: 3:

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGCGGCTATA AATGAAGAGG C

21

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Listeria monocytogenes*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATCCGATGAT GCTATGGCTT T

21

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Neisseria meningitidis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCAGCGGTAT TGTTTGGTGG T

21

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Neisseria meningitidis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CAGGCGGCCT TTAATAATTT C

21

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Staphylococcus saprophyticus*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AGATCGAATT CCACATGAAG GTTATTATGA

30

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Staphylococcus saprophyticus*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TCGCTTCTCC CTCAACAATC AAACATCCT

30

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus agalactiae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTTCACCAGC TGTATTAGAA GTA

23

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus agalactiae*

009964112001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GTTCCCTGAA CATTATCTTT GAT

23

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CAAGAAGGTT GGTACAACC CAAAGA

26

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AGGTCTTACC AGTAACTTTA CCGGAT

26

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TACTGACAAA CCATTCATGA TG

22

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

1002111 14968860

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AACTTCGTCA CCAACGCGAA C

21

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTGGCGCGGT ATGGTCGGTT

20

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GCCGACGTTG GAAGTGGTAA AG

22

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CCGTGTTGAA CGTGGTCAAA TCAA

25

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs

(ii) MOLECULE TYPE: DNA (genomic)

TRTGTGGTGT RATWGWCCA GGAGC

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ACAACGTGGW CAAGTWTTAG CWGCT

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ACCATTTCWG TACCTTCTGG TAAGT

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

```
(A) NAME/KEY: misc_feature
(B) LOCATION:12
(D) OTHER INFORMATION:/note= "n = inosine"
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GAAATTGCAG GNAAATTGAT TGA

23

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TTACGCATGG CNTGACTCAT CAT

23

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:3
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:9
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:15
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

099064 1 2495850

ACNKKNACNG GNGTNGARAT GTT

23

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:6
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:9
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:12
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:18
 - (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

AYRTTNTCNC CNGGCATNAC CAT

23

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TCGCTTCTCC

10

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 600 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TTCTTAGAGA CATTGAATAT GCCTTATGTC GGCGCAGGCG TATTGACCAG TGCATGTGCC 60
ATGGATAAAA TCATGACCAA GTATATTTTA CAAGCTGCTG GTGTGCCGCA AGTTCCTTAT 120
GTACCACTAC TTAAGAATCA ATGGAAAGAA AATCCTAAAA AAGTATTTGA TCAATGTGAA 180
GGTTCTTTGC TTTATCCGAT GTTTGTCAAA CCTGCGAATA TGGGTTCTAG TGTCGGCATT 240
ACAAAGGCAG AAAACCGAGA AGAGCTGCAA AATGCTTTAG CAACAGCCTA TCAGTATGAT 300
TCTCGAGCAA TCGTTGAACA AGGAATTGAA GCGCGCGAAA TCGAAGTTGC TGTATTAGGA 360
AATGAAGATG TTCGGACGAC TTTCCTGGC GAAGTCGTAA AAGACGTAGC ATTCTATGAT 420
TATGAAGCCA AATATATCAA TAATAAAATC GAAATGCAGA TTCCAGCCGA AGTGCCGGAA 480
GAAGTTTATC AAAAAGCGCA AGAGTACGCG AAGTTAGCTT ACACGATGTT AGGTGGAAGC 540
GGATTGAGCC GGTGCGATTT CTTTTTGACA AATAAAAATG AATTATTCCT GAATGAATTA 600

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1920 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GTGGGATTAA ACAGATTTAT GCGTGCGATG ATGGTGGTTT TCATTACTGC CAATTGCATT 60
ACGATTAACC CCGACATAAT ATTTGCAGCG ACAGATAGCG AAGATTCTAG TCTAAACACA 120
GATGAATGGG AAGAAGAAAA AACAGAAGAG CAACCAAGCG AGGTAAATAC GGGACCAAGA 180
TACGAACTG CACGTGAAGT AAGTTCACGT GATATTAAAG AACTAGAAAA ATCGAATAAA 240
GTGAGAAATA CGAACAAAGC AGACCTAATA GCAATGTTGA AAGAAAAAGC AGAAAAAGGT 300
CCAAATATCA ATAATAACAA CAGTGAACAA ACTGAGAATG CGGCTATAAA TGAAGAGGCT 360

TCAGGAGCCG ACCGACCAGC TATACAAGTG GAGCGTCGTC ATCCAGGATT GCCATCGGAT 420
 AGCGCAGCGG AAATTAAAAA AAGAAGGAAA GCCATAGCAT CATCGGATAG TGAGCTTGAA 480
 AGCCTTACTT ATCCGGATAA ACCAACAAAA GTAAATAAGA AAAAAGTGGC GAAAGAGTCA 540
 GTTGCGGATG CTTCTGAAAG TGAATTAGAT TCTAGCATGC AGTCAGCAGA TGAGTCTTCA 600
 CCACAACCTT TAAAAGCAAA CCAACAACCA TTTTCCCTA AAGTATTTAA AAAAATAAAA 660
 GATGCGGGGA AATGGGTACG TGATAAAATC GACGAAAATC CTGAAGTAAA GAAAGCGATT 720
 GTTGATAAAA GTGCAGGGTT AATTGACCAA TTATTAACCA AAAAGAAAAG TGAAGAGGTA 780
 AATGCTTCGG ACTTCCCGCC ACCACCTACG GATGAAGAGT TAAGACTTGC TTTGCCAGAG 840
 ACACCAATGC TTCTTGTTTT TAATGCTCCT GCTACATCAG AACCGAGCTC ATTCGAATTT 900
 CCACCACCAC CTACGGATGA AGAGTTAAGA CTTGCTTTGC CAGAGACGCC AATGCTTCTT 960
 GGTTTTAATG CTCTTGCTAC ATCGGAACCG AGCTCGTTTCG AATTTCCACC GCCTCCAACA 1020
 GAAGATGAAC TAGAAATCAT CCGGGAAACA GCATCCTCGC TAGATTCTAG TTTTACAAGA 1080
 GGGGATTTAG CTAGTTTGAG AAATGCTATT AATCGCCATA GTCAAAATTT CTCTGATTTT 1140
 CCACCAATCC CAACAGAAGA AGAGTTGAAC GGGAGAGGCG GTAGACCAAC ATCTGAAGAA 1200
 TTTAGTTCGC TGAATAGTGG TGATTTTACA GATGACGAAA ACAGCGAGAC AACAGAAGAA 1260
 GAAATTGATC GCCTAGCTGA TTTAAGAGAT AGAGGAACAG GAAAACACTC AAGAAATGCG 1320
 GGTTTTTTAC CATTAAATCC GTTTGCTAGC AGCCCGGTTT CTTCTGTTAAG TCCAAGGTA 1380
 TCGAAAATAA GCGACCGGGC TCTGATAAGT GACATAACTA AAAAAACGCC ATTTAAGAAT 1440
 CCATCACAGC CATTAAATGT GTTTAATAAA AAAACTACAA CGAAAACAGT GACTAAAAAA 1500
 CCAACCCCTG TAAAGACCGC ACCAAAGCTA GCAGAACTTC CTGCCACAAA ACCACAAGAA 1560
 ACCGTACTTA GGGAAAATAA AACACCCTTT ATAGAAAAAC AAGCAGAAAC AAACAAGCAG 1620
 TCAATTAATA TGCCGAGCCT ACCAGTAATC CAAAAAGAAG CTACAGAGAG CGATAAAGAG 1680
 GAAATGAAAC CACAAACCGA GGAAAAAATG GTAGAGGAAA GCGAATCAGC TAATAACGCA 1740
 AACGGAAAAA ATCGTTCTGC TGGCATTGAA GAAGGAAAAC TAATTGCTAA AAGTGCAGAA 1800
 GACGAAAAAG CGAAGGAAGA ACCAGGGAAC CATACGACGT TAATTCCTGC AATGTTAGCT 1860
 ATTGGCGTGT TCTCTTTAGG GCGGTTTATC AAAATTATTC AATTAAGAAA AAATAATTAA 1920

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 415 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TACCGGTACG CTAAATATTG GTGATGTATT GGATATTATG ATTTGGGAAG CGCCGCCAGC	60
GGTATTGTTT GGTGGTGGCC TTTCTTCGAT GGGCTCGGGT AGTGCGCAAC AAACCAAGTT	120
GCCGGAGCAA CTGGTGACGG CACGTGGTAC GGTTCCTGTG CCGTTTGTTG GCGATATTTC	180
GGTGGTCGGT AAAACGCCTG GTCAGGTTCA GGAAATTATT AAAGGCCGCC TGAAAAAAT	240
GGCCAATCAG CCGCAAGTGA TGGTGCCTT GGTGCAGAAT AATGCGGCAA ATGTATCGGT	300
GATTCGCGCA GGCAATAGTG TCGGTATGCC GTTGACGGCA GCCGGTGAGC GTGTGTTGGA	360
TGCGGTGGCT GCGGTAGGTG GTTCAACGGC AAATGTGCAG GATACGAATG TGCAG	415

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TCGCTTCTCC AGAAGAAATT TTAGAAACAT ATCTAGAAAA TCCCAAATTA GATAAACCGT	60
TTATATTATG TGAATACGCA CATGCAATGG GAAATTCACC AGGAGATCTT AATGCATATC	120
AAACATTAAT TGAAAAATAT GATAGTTTTA TTGGCGGTTT TGTTTGGGAA TGGTGTGATC	180
ATAGCATTCA GGTTGGGATA AAGGAAGGTA AACCAATTTT TAGATATGGT GGAGATTTTG	240
GTGAGGCCTT ACATGACGGT AATTTTTGTG TTGATGGTAT TGTTTCGCCA GATCGAATTC	300
CACATGAAGG TTATTATGAG TTAAACATG AACATAGACC TTTGAGATTG GTTAACGAAG	360
AGGATTATCG GTTTACATTG AAGAATCAAT TTGATTTTAC AAATGCGGAG GATAGTTTGA	420
TTGTTGAGGG AGAAGCGA	438

09090643-42004

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

ATGAACGTTA CACATATGAT GTATCTATCT GGAACTCTAG TGGCTGGTGC ATTGTTATTT 60
TCACCAGCTG TATTAGAAAGT ACATGCTGAT CAAGTGACAA CTCCACAAGT GGTAAATCAT 120
GTAAATAGTA ATAATCAAGC CCAGCAAATG GCTCAAAGC TTGATCAAGA TAGCATTTCAG 180
TTGAGAAATA TCAAAGATAA TGTTTCAGGA ACAGATTATG AAAAACCGGT TAATGAGGCT 240
ATTACTAGCG TGGAAAAATT AAAGACTTCA TTGCGTGCCA ACCCTGAGAC AGTTTATGAT 300
TTGAATTCTA TTGGTAGTCG TGTAGAAGCC TTAACAGATG TGATTGAAGC AATCACTTTT 360
TCAACTCAAC ATTTAACAAA TAAGGTTAGT CAAGCAAATA TTGATATGGG ATTTGGGATA 420
ACTAAGCTAG TTATTCGCAT TTTAGATCCA TTTGCTTCAG TTGATTCAAT TAAAGCTCAA 480
GTTAACGATG TAAAGGCATT AGAACAAAAA GTTTTAACTT ATCCTGATTT AAAACCAACT 540
GATAGAGCTA CCATCTATAC AAAATCAAAA CTTGATAAGG AAATCTGGAA TACACGCTTT 600
ACTAGAGATA AAAAAGTACT TAACGTCAAA GAATTTAAAG TTTACAATAC TTAAATAAAA 660
GCAATCACAC ATGCTGTTGG AGTTCAGTTG AATCCAAATG TTACGGTACA ACAAGTTGAT 720
CAAGAGATTG TAACATTACA AGCAGCACTT CAAACAGCAT TAAATAA 768

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATGAAAGTAG GTTTCGTCGG CTGGCGCGGT ATGGTCGGTT CGGTTTTGAT GCAGCGTATG 60
AAAGAAGAAA ACGACTTCGC CCACATTCCC GAAGCGTTTT TCTTTACCAC TTCCAACGTC 120
GGCGGCGCAC GCCCTGATTT CGGTCAGGCG GCTAAAACAT TATTGGACGC GAACAACGTT 180
GCCGAGCTGG CAAAAATGGA CATCATCGTT ACCTGCCAAG GCGGCGACTA CACCAAATCC 240
GTCTTCCAAG CCCTGCGCGA CAGCGGCTGG AACGGCTACT GGATTGACGC GGCATCCTCG 300
CTGCGTATGA AAGACGACGC GATTATCGTC CTCGACCCCG TCAACCGCAA CGTCATCGAC 360
AACGGCCTCA AAAACGGCGT GAAAACTAC ATCGGCGGCA ACTGTACCGT TTCCCTGATG 420
C 421

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

TTCATAGACG CTGAGCACGC TTTGGATCCA TCTTACGCGG CTGCTCTAGG TGTAATATT 60
GATGAGCTGT TGCTATCTCA ACCAGATTCT GGTGAGCAAG GTTTAGAAAT TGCAGGAAAA 120
TTGATTGACT CTGGGGCAGT TGATTTAGTT GTCATCGACT CTGTTGCAGC TCTTGTACCA 180
CGTGCGGAAA TCGATGGAGA TATCGGTGAT AGC 213

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GGGCCGGAAT CTTCTGGTAA GACAACTGTC GCTCTTCATG CTGCTGCTCA GGCGCAAAAA 60

09090543 11004
T002T E49000

GATGGCGGTA TTGCCGCTTT CATTGATGCA GAACATGCCC TTGATCCAGC CTATGCTGCT 120
 GCTCTTGGCG TTAATATTGA TGAGCTTTTG CTTTCACAAC CAGATTCAGG AGAACAGGGT 180
 CTTGAAATTG CAGGGAAATT GATTGATTCT GGCGCTGTTG ATTTAGTTGT TGTTGACTCA 240
 GTGGCAGCTT TAGTACCACG TGCGGAGATT GACGGAGATA TTGGTAATAG TCATGTTGGC 300
 TTACAAGCAC GCATGATGAG TCAAGCGATG CGTAAATTAT CAGCTTCAAT CAATAAAACA 360
 AAAACCATTG CTATTTTTAT TAATCAATTG CGGGAAAAAG TTGGTATTAT GTTTGGTAAT 420
 CCAGAAACAA CCCCTGGCGG GCGTGCCTTG AAGTTTTATT CTTCTGTGCG TCTTGATGTC 480
 CGCGGCAATA CTCAAATTAA AGGAACCGGG GAACAAAAAG ACAGCAATAT TGGTAAAGAG 540
 ACCAAAATTA AAGTTGTTAA AAATAAAGTT GCTCCACCAT TTAAGGAAGC TTTTGTAGAA 600
 ATTATATATG GTGAAGGCAT TTCTCGTACA GGTGAATTAG TTAAGATTGC CAGTGATTG 660
 GGAATTATCC AAAAAGCTGG AGCTTGGTAC TC 692

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

ATGGCGAAAA AACCAAAAAA ATTAGAAGAA ATTTCAAAAA AATTGGGGC AGAACGTGAA 60
 AAGGCCTTGA ATGACGCTCT TAAATTGATT GAGAAAGACT TTGGTAAAGG ATCAATCATG 120
 CGTTTGGGTG AACGTGCGGA GCAAAGGTG CAAGTGATGA GCTCAGGTTC TTTAGCTCTT 180
 GACATTGCCC TTGGCTCAGG TGTTATCCT AAGGGACGTA TCATCGAAAT CTATGGCCCA 240
 GAGTCATCTG GTAAGACAAC GGTGCCCCTT CATGCAGTTG CACAAGCGCA AAAAGAAGGT 300
 GGGATTGCTG CCTTTATCGA TGCGGAACAT GCCCTTGATC CAGCTTATGC TGCGGCCCTT 360
 GGTGTCAATA TTGACGAATT GCTCTTGTCT CAACCAGACT CAGGAGAGCA AGGTCTTGAG 420
 ATTGCGGGAA AATTGATTGA CTCAGGTGCA GTTGATCTTG TCGTAGTCGA CTCAGTTGCT 480
 GCCCTTGTTT CTCGTGCGGA AATTGATGGA GATATCGGAG ATAGCCATGT TGGTTTGCAG 540
 GCTCGTATGA TGAGCCAGGC CATGCGTAAA CTTGGCGCCT CTATCAATAA AACCAAAACA 600

ATTGCCATTT TTATCAACCA ATTGCGTGAA AAAGTTGGAG TGATGTTTGG AAATCCAGAA	660
ACAACACCGG GCGGACGTGC TTTGAAATTC TATGCTTCAG TCCGCTTGGA TGTTCTGGT	720
AATACACAAA TTAAGGGAAC TGGTGATCAA AAAGAAACCA ATGTCGGTAA AGAACTAAG	780
ATTAAGGTTG TAAAAAATAA GGTAGCTCCA CCGTTTAAGG AAGCCGTAGT TGAAATTATG	840
TACGGAGAAG GAATTTCTAA GACTGGTGAG CTTTTGAAGA TTGCAAGCGA TTTGGATATT	900
ATCAAAAAAG CAGGGGCTTG GTATTCTTAC AAAGATGAAA AAATTGGGCA AGGTTCTGAG	960
AATGCTAAGA AATACTTGGC AGAGCACCCA GAAATCTTTG ATGAAATTGA TAAGCAAGTC	1020
CGTTCTAAAT TTGGCTTGAT TGATGGAGAA GAAGTTTCAG AACAGATAC TGAAAACAAA	1080
AAAGATGAGC CAAAGAAAGA AGAAGCAGTG AATGAAGAAG TTCCGCTTGA CTTAGGCGAT	1140
GAACTTGAAA TCGAAATTGA AGAATAAGCT GTTAAAGCAG TGGAGAAATC CGCTACTTTT	1200
TCGA	1204

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATGCGTTCAG GAAGTCTAGC TCTTGATATT GCTTGGATAG CTGGTGGTTA TCCTAAAGGA	60
CGTATCATCG AAATCTATGG TCCAGAGTCT TCCGGTAAAA CGACTGTGGC TTTACATGCT	120
GTAGCACAAG CTCAAAAAGA AGGTGGAATC GCAGCCTTTA TCGATGCCGA GCATGCGCTT	180
GATCCAGCTT ATGCTGCTGC GCTTGGGGTT AATATTGATG AACTTCTCTT GTCTCAACCA	240
GATTCTGGAG AACAGGACT TGAAATTGCA GGTAAATTGA TTGATTCTGG TCGGTTGAC	300
CTGGTTGTTG TCGATTCACT AGCAGCTTTA GTGCCACGTG CTGAAATTGA TGGTGATATT	360
GGCGATAGCC ATGTCGGATT GCAAGCACGT ATGATGAGTC AGGCCATGCG TAAATTATCA	420
GCTTCTATTA ATAAAACAAA AACTATCGCA ATCTTTATCA ACCAATTGCG TGAAAAAGTT	480
GGTGTGATGT TTGGAAATCC TGAAACAACA CCAGGTGGTC GAGCTTTGAA ATTCTATGCT	540
TCTGTTCCGC TGGATGTGCG TGGAAACAAC CAAATTAAAG GAACTGGTGA CCAAAGATA	600

GCCAGCATTG GTAAGGAGAC CAAAATCAAG GTTGTTAAAA ACAAGGTCGC TCCGCCATTT	660
AAGGTAGCAG AAGTTGAAAT CATGTATGGG GAAGGTATTT CTCGTACAGG GGAGCTTGTG	720
AAAATTGCTT CTGATTTGGA CATTATCCAA AAAGCAGGTG CTTGGTTCTC TTATAATGGT	780
GAGAAGATTG GCCAAGGTTT TGAAAATGCT AAGCGTTATT TGGCCGATCA TCCACAATTG	840
TTTGATGAAA TCGACCGTAA AGTACGTGTT AAATTTGGTT TGCTTGAAGA AAGCGAAGAA	900
GAATCTGCTA TGGCAGTAGC ATCAGAAGAA ACCGATGATC TTGCTTTAGA TTTAGATAAT	960
GGTATTGAAA TTGAAGATTA A	981

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GCGTATGCAC GAGCTCTAGG TGTTAATATC GATGAGCTTC TTTTGTCGCA GCCTGATTCT	60
GGTGAGCAAG GTCTCGAAAT TGCAGGTAAG CTGATTGACT CTGGTGCACT GGATTTAGTT	120
GTTGTTGACT CAGTTGCGGC CTTTCGTACCA CGTGCAGAAA TTGATGGAGA TAGTGGTGAC	180
AGTCATGTAG GACTTCAAGC GCGTATGATG AGTCAAGCCA TGCGTAAACT TTCTGCATCT	240
ATTAATAAAA CAAAACGAT TGCTATCTTT ATTAACCACT TGCCTGAAAA AGTTGGTATC	300
ATGTTTGGA AC	312

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CTATGTGGCG CGGTATTATC

20

(2) INFORMATION FOR SEQ ID NO: 38:

(ii) MOLECULE TYPE: DNA (genomic)

CGCAGTGTTA TCACTCATGG

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTGAATGAAG CCATACCAA

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

ATCAGCAATA AACCCAGCCAG

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

TTACCATGAG CGATAACAGC

20

(2) INFORMATION FOR SEQ ID NO: 42:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

20

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

TTGAATTTGG CTTCTTCGGT

20

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGGATACAGA AACGGGACAT

20

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

TAAATCTTTT TCAGGCAGCG

20

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GATGGTTTGA AGGGTTTATT ATAAG

25

(2) INFORMATION FOR SEQ ID NO: 50:

009064 4303
"TCTT" 436660

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

CAGCTGTTAC AACGGACTGG

20

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TCTATGATCT CGCAGTCTCC

20

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

ATCGTCACCG TAATCTGCTT

20

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CATTCTCGAT TGCTTTGCTA

20

(2) INFORMATION FOR SEQ ID NO: 58:

099894 1000
T0027 1498660

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CCGAAATGCT TCTCAAGATA

20

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

CTGGATTATG GCTACGGAGT

20

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

AGCAGTGTGA TGGTATCCAG

20

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACTCTTGAT GAAGTGCTGG

20

(2) INFORMATION FOR SEQ ID NO: 62:

039094-1300
T002T-490000

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

CTGGTCTATT CCTCGCACTC

20

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

TATGAGAAGG CAGGATTCGT

20

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GCTTTCTCTC GAAGGCTTGT

20

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GAGTTGCTGT TCAATGATCC

20

(2) INFORMATION FOR SEQ ID NO: 66:

09080643 112001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

20

(2) INFORMATION FOR SEQ ID NO: 70:

(ii) MOLECULE TYPE: DNA (genomic)

TGCTGTCATA TTGTCTTGCC

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ATTATCTTCG GCGGTTGCTC

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

GACTATCGGC TTCCCATTC

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CGATAGAAGC AGCAGGACAA

20

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

CTGATGGATG CGGAAGATAC

20

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GCCTTATGTA TGAACAAATG G

21

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

GTGACTTTWG TGATCCCTTT TGA

23

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

TCCAATCATT GCACAAAATC

20

(2) INFORMATION FOR SEQ ID NO: 78:

0908064 11001

(ii) MOLECULE TYPE: DNA (genomic)

AATTCCCTCT ATTTGGTGGT

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TCCCAAGCCA GTAAAGCTAA

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

TGGTTTTTCA ACTTCTTCCA

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

TCATAGAATG GATGGCTCAA

20

(2) INFORMATION FOR SEQ ID NO: 82:

(2) INFORMATION FOR SEQ ID NO: 86:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

CCTTTACTCC AATAATTGG CT

22

(2) INFORMATION FOR SEQ ID NO: 87:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

TTTCATCTAT TCAGGATGGG

20

(2) INFORMATION FOR SEQ ID NO: 88:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GGAGCAACAT TCTTTGTGAC

20

(2) INFORMATION FOR SEQ ID NO: 89:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TGTGCCTGAA GAAGGTATTG

20

(2) INFORMATION FOR SEQ ID NO: 90:

(ii) MOLECULE TYPE: DNA (genomic)

CGTGTTACTT CACCACCACT

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

TATCTTATCG TTGAGAAGGG ATT

23

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CTACACTTGG CTTAGGATGA AA

22

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CTATCTGATT GTTGAAGAAG GATT

24

(2) INFORMATION FOR SEQ ID NO: 94:

(ii) MOLECULE TYPE: DNA (genomic)

GTTTACTCTT GGTTCAGGAT GAAA

24

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CTTGTTGATC ACGATAATT CC

22

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

ATCTTTTAGC AAACCCGTAT TC

22

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

AACAGGTGAA TTATTAGCAC TTGTAAG

27

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

ATTGCTGTGA ATATTTTTTG AGTTGAA

27

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

GTGATCGAAA TCCAGATCC

19

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

ATCCTCGGTT TTCTGGAAG

19

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CTGGTCATAC ATGTGATGG

19

(2) INFORMATION FOR SEQ ID NO: 102:

FOOTNOTES 4958550

(ii) MOLECULE TYPE: DNA (genomic)

GATGTTACCC GAGAGCTTG

19

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

TTAAGCGTGC ATAATAAGCC

20

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

TTGCGATTAC TTCGCCAACT

20

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

TTTACTAAGC TTGCCCCTTC

20

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

AAAAGGCAGC AATTATGAGC

20

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:9
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:12
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:15
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:18
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:21
 - (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

AAAYATGATNA CNGGNGCNGC NCARATGGA

29

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:3
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:9
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CCNACNGTNC KNCCRCCYTC RCG

23

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:15
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

009964 1200
000000 04968600

(B) LOCATION:18

(D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CARYTNATHG TNGCNGTNAA YAARATGGA

29

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

ATGAAAAACA CAATACATAT CAACTTCGCT ATTTTTTTTAA TAATTGCAAA TATTATCTAC 60
AGCAGCGCCA GTGCATCAAC AGATATCTCT ACTGTTGCAT CTCCATTATT TGAAGGAACT 120
GAAGGTTGTT TTTTACTTTA CGATGCATCC ACAAACGCTG AAATTGCTCA ATTCAATAAA 180
GCAAAGTGTG CAACGCAAAT GGCACCAGAT TCAACTTTCA AGATCGCATT ATCACTTATG 240
GCATTTGATG CGGAAATAAT AGATCAGAAA ACCATATTCA AATGGGATAA AACCCCCAAA 300
GGAATGGAGA TCTGGAACAG CAATCATACA CCAAAGACGT GGATGCAATT TTCTGTTGTT 360
TGGGTTTCGC AAGAAATAAC CCAAAAAATT AGATTAAATA AAATCAAGAA TTATCTCAAA 420
GATTTTGATT ATGGAAATCA AGACTTCTCT GGAGATAAAG AAAGAAACAA CGGATTAACA 480
GAAGCATGGC TCGAAAGTAG CTTAAAAATT TCACCAGAAG AACAAATTCA ATTCCTGCGT 540
AAAATTATTA ATCACAATCT CCCAGTTAAA AACTCAGCCA TAGAAAACAC CATAGAGAAC 600
ATGTATCTAC AAGATCTGGA TAATAGTACA AAAGTGTATG GGAAACTGG TGCAGGATTC 660
ACAGCAAATA GAACCTTACA AAACGGATGG TTTGAAGGGT TTATTATAAG CAAATCAGGA 720
CATAAATATG TTTTGTGTC CGCACTTACA GGAACTTGG GGTCGAATTT AACATCAAGC 780
ATAAAAGCCA AGAAAAATGC GATCACCATT CTAAACACAC TAAATTTATA A 831

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

19991114 14:56:57

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

TTGAAAAAGT TAATATTTTT AATTGTAATT GCTTTAGTTT TAAGTGCATG TAATTCAAAC	60
AGTTCACATG CCAAAGAGTT AAATGATTTA GAAAAAAAT ATAATGCTCA TATTGGTGT	120
TATGCTTTAG ATACTAAAAG TGGTAAGGAA GTAAAATTTA ATTCAGATAA GAGATTTGCC	180
TATGCTTCAA CTTCAAAGC GATAAATAGT GCTATTTTGT TAGAACAAGT ACCTTATAAT	240
AAGTTAAATA AAAAAGTACA TATTAACAAA GATGATATAG TTGCTTATTC TCCTATTTTA	300
GAAAAATATG TAGGAAAAGA TATCACTTTA AAAGCACTTA TTGAGGCTTC AATGACATAT	360
AGTGATAATA CAGCAAACAA TAAATTATA AAAGAAATCG GTGGAATCAA AAAAGTTAAA	420
CAACGTCTAA AAGAACTAGG AGATAAGTA ACAAATCCAG TTAGATATGA GATAGAATTA	480
AATTACTATT CACCAAAGAG CAAAAAGAT ACTTCAACAC CTGCTGCTTT CGGTAAGACT	540
TTAAATAAAC TTATCGCAA TGGAAAATTA AGCAAAGAAA AAAAAAATT CTTACTTGAT	600
TTAATGTAA ATAATAAAG CGGAGATACT TTAATTAAAG ACGGTGTTCC AAAAGACTAT	660
AAGGTTGCTG ATAAAAGTGG TCAAGCAATA ACATATGCTT CTAGAAATGA TGTGCTTTT	720
GTTTATCCTA AGGGCCAATC TGAACCTATT GTTTTAGTCA TTTTACGAA TAAAGACAAT	780
AAAAGTGATA AGCCAAATGA TAAGTTGATA AGTGAAACCG CCAAGAGTGT AATGAAGGAA	840
TTTTAA	846

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

ATGTCCGCGA GCACCCCCC CATAACTCTT CGCCTCATGA CCGAGCGCGA CCTGCCGATG	60
CTCCATGACT GGCTCAACCG GCCGCACATC GTTGAGTGGT GGGGTGGCGA CGAAGAGCGA	120
CCGACTCTTG ATGAAGTGCT GGAACACTAC CTGCCCAGAG CGATGGCGGA AGAGTCCGTA	180
ACACCGTACA TCGCAATGCT GGGCGAGGAA CCGATCGGCT ATGCTCAGTC GTACGTCGCG	240
CTCGGAAGCG GTGATGGCTG GTGGGAAGAT GAACTGATC CAGGAGTGCG AGGAATAGAC	300
CAGTCTCTGG CTGACCCGAC ACAGTTGAAC AAAGGCCTAG GAACAAGGCT TGTCCGCGCT	360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

ATGAACAAAA ATATAAAATA TTCTCAAAC TTTTAAACGA GTGAAAAAGT ACTCAACCAA 60
ATAATAAAAC AATTGAATTT AAAAGAAACC GATACCGTTT ACGAAATTGG AACAGGTAAA 120
GGGCATTTAA CGACGAAACT GGCTAAAATA AGTAAACAGG TAACGTCTAT TGAATTAGAC 180
AGTCATCTAT TCAACTTATC GTCAGAAAAA TTAAAATCGA ATACTCGTGT CACTTTAATT 240
CACCAAGATA TTCTACAGTT TCAATTCCCT AACAAACAGA GGTATAAAAT TGTTGGGAAT 300
ATTCCCTTACC ATTTAAGCAC ACAAATTATT AAAAAAGTGG TTTTGAAG CCATGCGTCT 360
GACATCTATC TGATTGTTGA AGAAGGATTC TACAAGCGTA CCTTGATAT TCACCGAACA 420
CTAGGGTTGC TCTTGCACAC TCAAGTCTCG ATTCAGCAAT TGCTTAAGCT GCCAGCGGAA 480
TGCTTTCATC CTAAACCAAG AGTAAACAGT GTCTTAATAA AACTTACCCG CCATACCACA 540
GATGTTCCAG ATAAATATTG GAAGCTATAT ACGTACTTTG TTTCAAATG GGTCAATCGA 600
GAATATCGTC AACTGTTTAC TAAAAATCAG TTTCATCAAG CAATGAAACA CGCCAAAGTA 660
AACAAATTAA GTACCGTTAC TTATGAGCAA GTATTGTCTA TTTTAAATAG TTATCTATTA 720
TTTAACGGGA GGAAATAA 738

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

ATGAACGAGA AAAATATAAA ACACAGTCAA AACTTTATTA CTTCAAACA TAATATAGAT 60
AAAATAATGA CAAATATAAG ATTAAATGAA CATGATAATA TCTTTGAAAT CGGCTCAGGA 120
AAAGGGCATT TTACCCTTGA ATTAGTACAG AGGTGTAATT TCGTAACTGC CATTGAAATA 180
GACCATAAAT TATGCAAAAC TACAGAAAAT AACTTGTTG ATCACGATAA TTTCCAAGTT 240
TTAAACAAGG ATATATTGCA GTTTAAATTT CCTAAAAACC AATCCTATAA AATATTTGGT 300
AATATACCTT ATAACATAAG TACGGATATA ATACGCAAAA TTGTTTTTGA TAGTATAGCT 360
GATGAGATTT ATTTAATCGT GGAATACGGG TTTGCTAAAA GATTATTAAA TACAAAACGC 420
TCATTGGCAT TATTTTAAAT GGCAGAAGTT GATATTTCTA TATTAAGTAT GGTTCCAAGA 480

0999643-112001

GAATATTTTC ATCCTAAACC TAGAGTGAAT AGCTCACTTA TCAGATTAAA TAGAAAAAAA	540
TCAAGAATAT CACACAAAGA TAAACAGAAG TATAATTATT TCGTTATGAA ATGGGTTAAC	600
AAAGAATACA AGAAAATATT TACAAAAAAT CAATTTAACA ATTCCTTAAA ACATGCAGGA	660
ATTGACGATT TAAACAATAT TAGCTTTGAA CAATTCTTAT CTCTTTTCAA TAGCTATAAA	720
TTATTTAATA AGTAA	735

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

ATGAATAAAA TAAAAGTCGC AATTATCTTC GGCGGTTGCT CGGAGGAACA TGATGTGTCG	60
GTAAAATCCG CAATAGAAAT TGCTGCGAAC ATTAATACTG AAAAATTCGA TCCGCACTAC	120
ATCGGAATTA CAAAAACGG CGTATGGAAG CTATGCAAGA AGCCATGTAC GGAATGGGAA	180
GCCGATAGTC TCCCCGCCAT ATTCTCCCCG GATAGGAAAA CGCATGGTCT GCTTGTCATG	240
AAAGAAAGAG AATACGAAAC TCGGCGTATT GACGTGGCTT TCCCGGTTTT GCATGGCAAA	300
TGCGGGGAGG ATGGTGCGAT ACAGGGTCTG TTTGAATTGT CTGGTATCCC CTATGTAGGC	360
TGCGATATTC AAAGCTCCGC AGCTTGCATG GACAAATCAC TGGCCTACAT TCTTACAAAA	420
AATGCGGGCA TCGCCGTCCC CGAATTTCOA ATGATTGAAA AAGGTGACAA ACCGGAGGCG	480
AGGACGCTTA CCTACCCTGT CTTTGTGAAG CCGGCACGGT CAGGTTTCGTC CTTTGGCGTA	540
ACCAAAGTAA ACAGTACGGA AGAACTAAAC GCTGCGATAG AAGCAGCAGG ACAATATGAT	600
GGAAAAATCT TAATTGAGCA AGCGATTTTCG GGCTGTGAGG TCGGCTGCGC GGTTCATGGGA	660
AACGAGGATG ATTTGATTGT CGGCGAAGTG GATCAAATCC GGTTGAGCCA CGGTATCTTC	720
CGCATCCATC AGGAAAACGA GCCGGAAAAA GGCTCAGAGA ATGCGATGAT TATCGTTCCA	780
GCAGACATTC CGGTGAGGA ACGAAATCGG GTGCAAGAAA CGGCAAAGAA AGTATATCGG	840
GTGCTTGAT GCAGAGGGCT TGCTCGTGTT GATCTTTTTT TGCAGGAGGA TGGCGGCATC	900
GTTCTAAACG AGGTCAATAC CCTGCCCCGT TTTACATCGT ACAGCCGCTA TCCACGCATG	960
GCGGCTGCCG CAGGAATCAC GCTTCCCGCA CTAATTGACA GCCTGATTAC ATTGGCGATA	1020

T0027-249850

GAGAGGTGA

1029

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATGAAAAAAAA TTGCCGTTTT ATTTGGAGGG AATTCTCCAG AATACTCAGT GTCACTAACC	60
TCAGCAGCAA GTGTGATCCA AGCTATTGAC CCGCTGAAAT ATGAAGTAAT GACCATTGGC	120
ATCGCACCAA CAATGGATTG GTATTGGTAT CAAGGAAACC TCGCGAATGT TCGCAATGAT	180
ACTTGGCTAG AAGATCACAA AAAGTGTAC CAGCTGACTT TTTCTAGCCA AGGATTTATA	240
TTAGGAGAAA AACGAATCGT CCCTGATGTC CTCTTTCCAG TCTTGCATGG GAAGTATGGC	300
GAGGATGGCT GTATCCAAGG ACTGCTTGAA CTAATGAACC TGCCTTATGT TGGTTGCCAT	360
GTCGCTGCCT CCGCATTATG TATGAACAAA TGGCTCTTGC ATCAACTTGC TGATACCATG	420
GGAATCGCTA GTGCTCCAC TTTGCTTTTA TCCCGCTATG AAAACGATCC TGCCACAATC	480
GATCGTTTTA TTCAAGACCA TGGATTCCCG ATCTTTATCA AGCCGAATGA AGCCGGTTCT	540
TCAAAAGGGA TCACAAAAGT AACTGACAAA ACAGCGCTCC AATCTGCATT AACGACTGCT	600
TTTGCTTACG GTTCTACTGT GTTGATCCAA AAGGCGATAG CGGGTATTGA AATTGGCTGC	660
GGCATCTTAG GAAATGAGCA ATTGACGATT GGTGCTTGTG ATGCGATTTC TCTTGTGAC	720
GGTTTTTTTG ATTTTGAAGA GAAATACCAA TTAATCAGCG CCACGATCAC TGTCCCAGCA	780
CCATTGCCTC TCGCGCTTGA ATCACAGATC AAGGAGCAGG CACAGCTGCT TTATCGAAAC	840
TTGGGATTGA CGGGTCTGGC TCGAATCGAT TTTTTCGTCA CCAATCAAGG AGCGATTAT	900
TTAAACGAAA TCAACACCAT GCCGGGATTT ACTGGGCACT CCCGCTACCC AGCTATGATG	960
GCGGAAGTCG GGTTATCCTA CGAAATATTA GTAGAGCAAT TGATTGCACT GGCAGAGGAG	1020
GACAAACGAT G	1031

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Abiotrophia adiacens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

TGGTGCTATC TTAGTAGTAT CTGCAGCTGA TGGTCCAATG CCTCAAACAC GTGAACACAT	60
CTTATTATCA CGTCAAGTAG GTGTTCCTTA CATCGTTGTA TTCTTAAACA AAGTTGACAT	120
GGTTGACGAT GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTATCAGA	180
ATACGATTTC CCAGGCGATG ACACTCCAGT TGTTCAGGT TCTGCTTTAC GCGCTTTAGA	240
AGGCGACGCT TCATACRAAG AAAAAATCTT AGAATTAATG GCTGCTGTTG ACGAATACAT	300
TCCAACCTCA GAACGYGACG TTGACAAACC ATTCATGATG CCAGTTGAAG ACGTGTTCCTC	360
AATCACAGGT CGTGGTACTG TTGCTACAGG TCGTGTGAA CGTGGACAAG TTCGTGTTGG	420
TGACGAAGTT GAAATCGTTG GTATTTTCTA AGAACTTCA AAAACAACCTG TAACTGGTGT	480
TGAAATGTTT CGTAAATTGT TAGACTACGC TGAAGCAGGG GATAACATTG GTACATTATT	540
ACGTGGTGTT ACACGTGACA ACATCGAAGT TGGACAAGTT CTTGCTAAAC CAGGAACAAT	600
CACTCCACAT ACTAAATTCA AAGCTGAAGT TTACGTATTA ACTAAGAAG AAGGTGGACG	660
TCATACTCCA TTCTTCTCTA ACTACCGTCC TCAATTCTAC TTCCGTACAA CAGACATCAC	720
TGGTGTTTGT GTGTTACCAG AAGGCGTTGA AATGGTAATG CCTGGTGATA ACGTAACTAT	780
GGAAGTTGAA TTAATTCACC CAGTAGCGA	809

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Abiotrophia defectiva*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

CGGCGCGATC CTCGTTGTAT CTGCTGCTGA CGGCCCAATG CCACAACTC GTGAACACAT	60
CCTCTTGTCT CGTCAAGTTG GTGTTCCTTA CATCGTAGTA TTCTTGAACA AAGTTGACAT	120

GGTTGACGAC GAAGAATTGC TCGAATTAGT TGAAATGGAA GTTCGTGACC TCTTGTCTGA 180
 ATACGACTTC CCAGGCGACG ACACTCCAGT TATCGCTGGT TCAGCTTTGA AAGCTTTAGA 240
 AGGCGACGCT AACTACGAAG CTAAAGTTTT AGAATTGATG GAACAAGTTG ATGCTTACAT 300
 TCCAGAACCA GAACGTGACA CTGACAAGCC ATTCATGATG CCAGTCGAAG ACGTATTCTC 360
 TATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTGAA CGTGGTCAAG TTCGCGTTGG 420
 TGACGAAGTT GAAATCGTTG GTATCGAAGA AGAACTTCT AAGACTACCG TTACCGGTGT 480
 TGAAATGTTC CGTAAGTTAT TGGATTACGC TGAAGCTGGG GACAACGTTG GTACCTTGTT 540
 ACGTGGTGTA ACTCGTGACC AAATCCAACG TGGTCAAGTA TTATCTAAAC CAGGTTCAAT 600
 CACTCCGYAC ACTAAGTTCG AAGCTGAAGT GTACGTATTG TCTAAAGAAG AAGGTGGTCG 660
 TCACACTCCA TTCTTCTCTA ACTACCGTCC ACAATTCTAC TTCCGTACAA CTGACGTAAC 720
 TGGTGTGTT ACTTTACCAG AAGGTACTGA AATGGTTATG CCAGGCGACA ACGTACAAAT 780
 GGTTGTTGAA TTGATCCACC CAATCGCGAT CGAAGAA 817

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

CTCTGTCAAA TGGGACAAAA ACAGATTTGA AGAAATCATC AAGGAAACCT CCAACTTCGT 60
 CAAGAAGGTT GGTTACAACC CAAAGACTGT TCCATTCGTT CCAATCTCTG GTTGGAATGG 120
 TGACAACWTG ATTGAASCAT CCACCAACTG TCCATGGTAC AAGGGTTGGG AAAAGGAAAC 180
 CAAATCCGGT AAAGTTACTG GTAAGACCTT GTTAGAAGCT ATTGACGCTA TTGAACCACC 240
 AACCAGACCA ACCGACAAAC CATTGAGATT GCCATTRCAA GATGTTTACA AGATCGGTGG 300
 TATTGGTACT GTGCCAGTCG GTAGAGTTGA AACTGGTATC ATCAAAGCCG GTATGGTWGT 360
 TACTTTCGCC CCAGCTGGTG TTACCACTGA AGTCAARTCC GTTGAAATGC ATCACGAACA 420
 ATTGGCTGAA GGTGTTCCAG GTGACAATGT TRGTTTCAAC GTTAAGAACR TTTCCGTAA 480
 AGAAATTAGA AGAGGTAACG TTTGTGGTGA CTCCAAGAAC GATCCACCAA AGGGTTGTGA 540

(2) INFORMATION FOR SEQ ID NO: 121:

(A) LENGTH: 753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 121:

(2) INFORMATION FOR SEQ ID NO: 122:

(A) LENGTH: 752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida krusei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

CCGTTAAGTG GGATGAAAAC AGATTTGAAG AAATTGTCAA GGAAACCCAA AACTTCATCA 60
AGAAGGTTGG TTACAACCCA AAGACTGTTT CATTCGTTCC AATCTCTGGT TGAATGGTG 120
ACAACATGAT TGAAGCATCC ACCAACTGTC CATGGTACAA GGGTTGGACT AAGGAAACCA 180
AGGCAGGTGT TGTTAAGGGT AAGACCTTAT TAGAAGCAAT CGATGCTATT GAACCACCTG 240
TCAGACCAAC CGAAAAGCCA TTAAGATTAC CATTACAAGA TGTTTACAAG ATTGGTGGTA 300
TTGGTACTGT GCCAGTCGGT AGAGTCGAAA CCGGTGTCAT TAAGCCAGGT ATGGTTGTCA 360
CTTTTGCTCC AGCAGGTGTC ACCACCGAAG TCAAATCCGT TGAAATGCAC CATGAACAAT 420
TAGAACAAGG TGTTCCAGGT GATAACGTTG GTTTCAACGT TAAGAACGTY TCTGTCAAGG 480
ATATCAAGAG AGGTAACGTT TGTGGTGAAT CCAAGAACGA CCCACCAATG GGTGCAGCTT 540
CTTTCAATGC TCAAGTCATT GTCTTGAACC ACCCTGGTCA AATTTCCGCT GGTTACTCTC 600
CAGTCTTGGA TTGTCACACT GCCCACATTG CATGTAAGTT CGACGAATTA ATCGAAAAGA 660
TTGACAGAAG AACTGGTAAG TCTGTTGAAG ACCATCCAAA GTCYGTCAAG TCTGGTGATG 720
CAGCTATCGT CAAGATGGTC CCAACCAAGC CA 752

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 754 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida parapsilosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CTCAGTCAAA TGGGACAAGA RCAGATACGA AGAAATTGTC AAGGAACTT CCAACTTCGT 60
CAAGAAGGTT GGTTACAACC CTAAAGCTGT CCCATTCGTC CCAATCTCTG GTTGGAAACGG 120
TGACAATATG ATTGAACCAT CAACCAACTG TCCATGGTAC AAGGGTTGGG AAAAGGAAAC 180
TAAAGCTGGT AAGGTTACCG GTAAGACCTT GTTGGAAAGCT ATCGATGCTA TCGARCCACC 240

(2) INFORMATION FOR SEO ID NO: 124:

(A) LENGTH: 753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida tropicalis*

TCTGTTAAAT	GGGACAARAA	CAGATTTGAA	GAAATTATCA	AGGAAACYTC	TAACTTCGTC	60
AAGAAGGTTG	GTTACAACCC	TAAGGCTGTT	CCATTCGTTT	CAATCTCWGG	TTGGAATGGT	120
GACAACATGA	TTGAAGCTTC	TACCAACTGT	CCATGGTACA	AGGGTTGGGA	AAAAGAAACC	180
AAGGCTGGTA	AGGTTACCGG	TAAGACTTTG	TTGGAAGCCA	TTGATGCTAT	TGAACCACCT	240
TCAAGACCAA	CTGACAAGCC	ATTGAGATTG	CCATTGCAAG	ATGTTTACAA	GATTGGTGGT	300
ATTGGTACTG	TGCCAGTCGG	TAGAGTTGAA	ACTGGTGTCA	TCAAAGCCGG	TATGGTTGTT	360
ACTTTYGCCC	CAGCTGGTGT	TACCACTGAA	GTCAAATCCG	TYGAAATGCA	CCACGAACAA	420
TTGGCTGAAG	GTGTCCCAGG	TGACAATGTT	GGTTTCAACG	TTAAGAACGT	TTCTGTTAAA	480
GAAATTAGAA	GAGGTAACGT	TTGTGGTGAC	TCCAAGAACG	ATCCACCAA	GGGTTGTGAC	540
TCTTTCAACG	CTCAAGTTAT	TGTCTTGAAC	CACCCAGGTC	AAATYTCTGC	TGGTTACTCT	600
CCAGTCTTGG	ATTGTCACAC	TGCTCATATT	GCTTGTAAT	TCGACACCTT	GGTTGAAAAG	660
ATTGACAGAA	GAAGTGGTAA	GAAATTGGAA	GAAAATCCAA	AATTCGTCAA	ATCCGGGTGAT	720

GCTGCTATTG TCAAGATGGT TCCAACCAAA CCA

753

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium accolens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

CGGCGCTATC CTGGTTGTTG CTGCAACCGA TGGCCCGATG CCGCAGACCC GCGAGCACGT	60
TCTGCTTGCT CGCCAGGTTG GCGTTCCTTA CATCCTCGTT GCACTGAACA AGTGCGACAT	120
GGTTGATGAT GAGGAAATCA TCGAGCTCGT GGAGATGGAG ATCTCCGAGC TGCTCGCAGA	180
GCAGGACTAC GATGAGGAAG CTCCTATCGT TCACATCTCC GCTCTGAAGG CACTCGAGGG	240
TGACGAGAAG TGGGTACAGT CCATCGTTGA CCTGATGGAT GCCTGCGACA ACTCCATCCC	300
TGATCCGGAG CGCGCTACCG ATCAGCCGTT CTTGATGCCT ATCGAGGACA TCTTCACCAT	360
TACCGGCCGC GGTACCGTTG TTACCGGCCG TGTGAGCGT GGTCTGTCTGA ACGTCAACGA	420
GGACGTTGAG ATCATCGGTA TCCAGGAGAA GTCCCAGAAC ACCACCGTTA CCGGTATCGA	480
GATGTTCCGC AAGATGATGG ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTGCG	540
TGGTACCAAG CGTGAGGACG TTGAGCGTGG CCAGGTTGTT ATCAAGCCGG GCGCTTACAC	600
CCCTCACACC AAGTTCGAGG GTTCCGTCTA CGTCCTGAAG AAGGAAGAGG GCGGCCGCCA	660
CACCCCGYTC ATGAACAACT ACCGTCCTCA GTTCTACTTC CGCACCACCG ACGTTACCGG	720
TGTTGTGAAC CTGCCTGAGG GCACCGAGAT GGTATGCCT GGCGACAACG TTGAGATGTC	780
TGTTGAGCTC ATCCAGCCTG TTGCTATGGA CGAG	814

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

0999643-12001

(A) ORGANISM: *Corynebacterium diphtheriae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

CGGCGCAATC CTCGTTGTTG CTGCCACCGA CGGCCCAATG CCTCAGACCC GTGAGCACGT 60
TCTGCTCGCT CGCCAGGTCG GCGTTCCTTA CATCCTCGTT GCTCTGAACA AGTGCGACAT 120
GGTTGATGAT GAGGAAATCA TCGAGCTCGT CGAGATGGAG ATCCRTGAGC TGCTCGCTGA 180
GCAGGATTAC GACGAAGAGG CTCCAATCAT CCACATCTCC GCACTGAAGG CTCTTGAGGG 240
CGACGAGAAG TGGACCCAGT CCATCATCGA CCTCATGCAG GCTTGCKATG ATTCCATCCC 300
AGACCCAGAG CGTGAGACCG ACAAGCCATT CCTCATGCCT ATCGAGGACA TCTTCACCAT 360
CACCGGCCGC GGTACCGTTG TTACCGGCCG TGTTGAGCGT GGCTCCCTGA AGGTCAACGA 420
GGACGTCGAG ATCATCGGTA TCCGCGAGAA KGCTACCACC ACCACCGTTA CCGGTATCGA 480
GATGTTCCGT AAGCTTCTCG ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTCCG 540
TGGCGTTAAG CGCGAAGACG TTGAGCGTGG CCAGGTTGTT GTTAAGCCAG GCGCTTACAC 600
CCCTCACACC GAGTTCGAGG GCTCTGTCTA CGTTCTGTCC AAGGACGAGG GTGGCCGCCA 660
CACCCCATTC TTCGACAACT ACCGCCACA GTTCTACTTC CGCACCACCG ACGTTACCGG 720
TGTTGTGAAG CTTCTGAGG GCACCGAGAT GGTCATGCCT GGCGACAACG TCGACATGTC 780
CGTCACCCTG ATCCAGCCTG TCGCTATGGA TGAG 814

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium genitalium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

CGGCGCCATC CTGGTTGTTG CTGCAACCGA TGGCCCGATG CCGCAGACCC GTGAGCACGT 60
TCTGCTGGCT CGCCAGGTTG GCGTTCGTA CATCCTAGTT GCACTGAACA AGTGCGACAT 120
GGTTGATGAT GAGGAGCTGC TGGAGCTCGT CGAGATGGAG GTCCGCGAGC TGCTGGCTGA 180
GCAGGACTTC GACGAGGAAG CACCTGTTGT TCACATCTCC GCACTGAAGG CCCTGGAGGG 240
CGACGAGAAG TGGGCTAAGC AGATCCTGGA GCTCATGGAG GCTTGCGACA ACTCCATCCC 300

GGATCCGGAG CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGRGGACA TCTTCACCAT	360
TACCGGCCGC GGTACCGTTG TTACCGGCCG TGTTGAGCGT GGCCTCCTGA ACCTGAACGA	420
CGAGGTCGAG ATCCTGGGCA TCCGCGAGAA GTCCACCAAG ACCACCGTTA CCTCCATCGA	480
GATGTTCAAC AAGCTGCTGG ACACCGCAGA GGCTGGCGAC AACGCCGCAC TGCTGCTGCG	540
TGGCCTGAAG CGCGAAGATG TTGAGCGTGG TCAGATCGTT GCTAAGCCGG GCGAGTACAC	600
CCCGCACACC GAGTTCGAGG GCTCCGTCTA CGTTCTGTCC AAGGACGAGG GTGGCCGCCA	660
CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTATTTC CGCACCACCG ACGTTACCGG	720
TGTTGTGAAG CTGCCGGAGG GCACCGAGAT GGTATGCCG GCGACAACG TTGACATGTC	780
CGTCACCCTG ATCCAGCCGG TTGCTATGGA CGAG	814

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium jeikeium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CGGCGCCATC CTGGTTGTTG CCGCAACCGA TGGCCCGATG CCGCAGACCC GCGAGCACGT	60
TCTGCTGGCY CGCCAGGTTG GCGTTCCGTA CATCCTGGTT GCACTGAACA AGTGTGACAT	120
GGTTGACGAT GAGGAGCTGC TGGAGCTCGT CGAGATGGAG GTCCGCGAGC TGCTGGCTGA	180
GCAGGACTTC GACGAGGAAG CTCCGGTTGT TCACATCTCC GCACTGAAGG CCCTGGAGGG	240
CGACGAGAAG TGGGCTAACC AGATTCTCGA GCTGATGCAG GCTTGCGACG AGTCTATCCC	300
GGATCCGGAG CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGWGGACA TCTTCACCAT	360
TACCGGTGCG GGTACCGTTG TTACCGGCCG TGTTGAGCGT GGCATCCTGA ACCTGAACGA	420
CGAGGTTGAG ATCCTGGGTA TCCGCGAGAA GTCCCAGAAG ACCACCGTTA CCTCCATCGA	480
GATGTTCAAC AAGCTGCTGG ACACCGCAGA GGCTGGCRAC AACGCTGCAC TGCTGCTGCG	540
TGGTCTGAAG CGCGAGGACG TTGAGCGTGG CCAGATCATC GCTAAGCCGG GCGAGTACAC	600
CCCGCACACC GAGTTCGAGG GCTCCGTCTA CGTTCTGTCC AAGGACGAGG GCGGCCGCCA	660
CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTACTTC CGCACCACCG ACGTTACCGG	720

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TGTTGTGAAG CTGCCTGAGG GCACCGAGAT GGTATGCCC GGCGACAACG TYGACATGTC 780
CGTCACCCTG ATCCAGCCGG TTGCTATGGA CGAG 814

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

CGGCGCTATC TTGGTTGTTG CAGCTACCGA CGGCCCAATG CCACAGACTC GCGAGCACGT 60
TCTGCTGGCT CGCCAGGTTG GCGTTCCTTA CATCCTGGTT GCACTAAACA AGTGCGACAT 120
GGTTGACGAC GAGGAAATCC TCGAGCTCGT CGAGATGGAG ATCCGCGAAT TGCTGGCTGA 180
CCAGGAATTC GACGAAGAAG CTCCAATCGT TCACATCTCC GCAGTCGGCG CCTTGAAGG 240
CGAAGAGAGG TGGGTAAACG CCATCGTTGA ACTGATGGAT GCTTGTGACG AGTCGATCCC 300
TGATCCAGAC CGTGCTACCG ACAAGCCATT CCTGATGCCT ATCGAGGACA TCTTCACCAT 360
TACCGGTCGT GGCACCGTTG TTACGGGTCTG TGTGAGCGT GGTCCCTGA AGGTCAACGA 420
AGAAGTCGAG ATCATCGGCA TCAAGGAAAA GTCCCAGAAG ACCACCATCA CCGGTATCGA 480
AATGTTCCGC AAGATGCTGG ACTACACCGA GGCCGGCGAC AACGCTGGTC TGCTGCTTCG 540
CGGTACCAAG CGTGAAGACG TTGAGCGTGG ACAGGTTATC GTTGCTCCAG GTGCTTACAG 600
CACCCACAAG AAGTTCGAAG GTTCCGTCTA CGTTCTTTCC AAGGACGAGG GCGGCCGCCA 660
CACCCCGTTC TTCGACAACT ACCGTCCTCA GTTCTACTTC CGCACCACCG ACGTTACCGG 720
TGTTGTTACC CTGCCTGAGG GCACCGAG 748

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium striatum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

GGCGCTATCT TGGTTGTTGC TGCAACCGAT GGCCCGRTGC CGCAGACCCG CGAGCACGTT 60
CTTCTGGCTC GCCAGGTTGG CGTTCCTTAC ATCCTCGTTG CACTGAACAA GTGCGACATG 120
GTTGACGACG AGGAAATTAT CGAGCTCGTC GAGATGGAGA TCCGCGAACT GCTCGCAGAG 180
CAGGACTACG ATGAGGAAGC TCCGATCGTT CACATCTCTG CTCTGAAGGC TCTTGAGGGC 240
GRCGAGAAGT GGGTACAGGC TATCGTTGAC CTGATGCAGG CTTGCGATGA CTCCATCCCG 300
GATCCGGAGC GCGAGCTGGA CAAGCCGTTT CTGATGCCAA TCGAGGACAT CTTACCATC 360
ACCGGCCGCG GTACCGTTGT TACTGGCCGT GTTGAGCGTG GCTCCCTGAA CGTCAACGAG 420
GACGTTGAGA TCATCGGTAT CCAGGACARG TCCATCTCCA CCACCGTTAC CGGTATCGAG 480
ATGYTCCGCA AGATGATGGA CTACACCGAG GCTGGCGACA ACTGTGGTCT GCTTCTGCGT 540
GGTACCAAGC GTGAAGAGGT TGAGCGCGGC CAGGTTGTTA TTAAGCCGGG CGCTTACACC 600
CCTCACACCC AGTTCGAGGG TTCCGTCTAC GTCCTGAAGA AGGAAGAGGG CGGCCGCCAC 660
ACCCCGTTCA TGGACAACTA CCGTCCGCAG TTCTACTTCC GCACCACCGA CGTTACCGGC 720
GTCATCAAGC TGCCTGAGGG CACCGAGATG GTTATGCCTG GCGACAACGT CGAGATGTCY 780
GTCGAGCTGA TCCAGCCGGT CGCTATGGAC GAG 813

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus avium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCTATG CCTCAAATC GTGAACACAT 60
CTTGTTATCT CGTAACGTTG GTGTTCTTA CATCGTTGTA TTCTTAAACA AAATGGATAT 120
GGTTGACGAT GAAGAATTAC TTGAATTAGT TGAAATGGAA GTTCGTGACT TATTAAGTGA 180
ATACGACTTC CCAGGCGACG AACTCCAGT TATCGCAGGT TCAGCGTTGA AAGCTTTAGA 240
AGGCGACGCT TCATACGAAG AAAAAATCTT AGAATTAATG GCTGCTGTTG ACGAATATAT 300

CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG ACGTATTCTC	360
AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTGAA CGTGGACAAG TTCGCGTTGG	420
TGACGAAGTT GAAATCGTAG GTATCGCTGA CGAAACTGCT AAAACAACCTG TTACAGGTGT	480
TGAAATGTTT CGTAAATTGT TAGACTACGC TGAAGCAGGT GACAACATCG GTGCTTTGTT	540
ACGTGGTGTT GCACGTGAAG ATATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT	600
CACTCCACAT ACAAATTCT CTGCAGAAGT TTATGTTCTA ACTAAGAAG AAGGTGGACG	660
TCATACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC TTCCGTACAA CTGACGTAAC	720
TGGTGTAGTT GATCTACCAG AAGGTACTGA AATGGTWTAG CCTGGGGATA ACGTAACTAT	780
GGAAGTTGAA TTGATYCACC CAATYCGGGT AGAAGAC	817

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGTCCTATG CCTCAAACAC GTGAACATAT	60
CTTATTATCA CGTAACGTTG GTGTACCATA CATCGTTGTA TTCTTAAACA AAATGGATAT	120
GGTTGATGAC GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTATCAGA	180
ATACGATTTC CCAGGCGATG ATGTTCCAGT TATCGCAGGT TCTGCTTTGA AAGCTTTAGA	240
AGGCGACGAG TCTTATGAAG AAAAAATCTT AGAATTAATG GCTGCAGTTG ACGAATATAT	300
CCCAACTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG ACGTATTCTC	360
AATCACTGGA CGTGGTACTG TTGCTACAGG ACGTGTGAA CGTGGTGAAG TTCGCGTTGG	420
TGACGAAGTT GAAATCGTTG GTATTAAAGA CGAAACATCT AAAACAACYG TTACAGGTGT	480
TGAAATGTTT CGTAAATTAT TAGACTACGC TGAAGCAGGC GACAACMTCG GTGCTTTATT	540
ACGTGGTGTA GCACGTGAAG ATATCGAACG TGGACAAGTA TTAGCTAAAC CAGCTACAAT	600
CACTCCACAC ACAAATTCA AAGCTGAAGT ATACGTATTA TCAAGAAG AAGGCGGACG	660
TCACACTCCA TTCTTCACTA ACTACCGTCC TCAATTCTAC TTCCGTACAA CAGACGTTAC	720

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TGGTGTGTA GAATTGCCAG AAGGTACTGA AATGGTAATG CCTGGTGATA ACGTTGCTAT 780
GGACGTTGAA TTAATTCACC CAATCGCTAT CGAAGAC 817

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CGGAGCTATC TTGGTAGTTT CTGCTGCTGA CGGCCCAATG CCTCAAACCTC GTGAACACAT 60
CCTATTGTCT CGTCAAGTTG GTGTTCCCTTA CATCGTTGTA TTCTTGAACA AAGTAGACAT 120
GGTTGATGAC GAAGAATTAC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTAACAGA 180
ATACRAATTC CCTGGTGRCG ATGTTCCCTGT AGTTGCTGGA TCAGCTTTGA AAGCTCTAGA 240
AGGCGACGCT TCATACGAAG AAAAAATTCT TGAATTAATG GCTGCAGTTG ACGAATACAT 300
CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTTGAAG ACGTGTTCCTC 360
AATTACTGGA CGTGGTACTG TTGCTACAGG TCGTGTTGAA CGTGGACAAG TTCGCGTTGG 420
TGACGAAGTT GAAGTTGTTG GTATTGCTGA AGAACTTCA AAAACAACAG TTACTGGTGT 480
TGAAATGTTT CGTAAATTGT TAGACYACGC TGAAGCTGGA GACRACATTG GTGCTTTACT 540
ACGTGGTGTT GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT 600
CACACCTCRT ACAAATTCT CTGCAGAAAGT ATACGTGTTG ACAAAGAAG AAGGTGGACG 660
TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC TTCCGTACAA CTGACGTAAC 720
AGGTGTTGTT GAATTACCAG AAGGAACTGA AATGGTCATG CCCGGTGACA ACGT 774

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

CGGTGCGATC TTAGTAGTAT CTGCTGCTGA CGGTCCTATG CCTCAAACCTC GTGAACACAT 60
CTTGTTATCA CGTAACGTTG GCGTACCATA CATCGTTGTT TTCTTGAACA AAATGGATAT 120
GGTTGAYGAC GAAGAATTGC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTGTCTGA 180
ATATGACTTC CCAGGCGACG ATGTTCTGT AATCGCCGGT TCTGCTTTGA AAGCTCTTGA 240
AGGAGATCCT TCATACGAAG AAAAAATCAT GGAATTGATG GCTGCAGTTG ACGAATACGT 300
TCCAACCTCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG ACGTATTCTC 360
AATCACTGGA CGTGGTACTG TTGCTACAGG CCGTGTTGAA CGTGGACAAG TTCGCGTTGG 420
TGATGAAGTA GAAATCGTTG GTATTGCTGA CGAACTGCT AAAACAACCTG TAACAGGTGT 480
TGAAATGTTC CGTAAATTGT TAGACTATGC TGAAGCAGGG GATAACATTG GTGCATTGCT 540
ACGTGGGGTT GCTCGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAG CTGGTACAAT 600
CACACCTCAT ACAAATTCA AAGCTGAAGT TTATGTTTTG ACAAAGAAG AAGGTGGACG 660
TCACACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC TTCCGTACAA CTGACGTAAC 720
TGGTGTGTT GAATTACCAG AAGGAACTGA AATGGTGATG CCTGGCGACA ACGTGACCAT 780
CGACGTTGAA TTGATRCACC CAATCGCTC 809

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gardnerella vaginalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

TGGCGCAATC CTCGTGGTTG CTGCTACCGA CGGTCCAATG GCTCAGACCC GTGAACACGT 60
CTTGCTTGCT AAGCAGGTCG GCGTTCCAAA AATTCTTGTT GCTTTGAACA AGTGCGATAT 120
GGTTGACGAC GAAGAGCTTA TCGATCTCGT TGAAGAAGAG GTCCGTGACC TCCTCGAAGA 180
AAACGGCTTC GATCGCGATT GCCCAGTCYT CCGTACTTCC GCTTACGGCG CTTTGCATGA 240
TGACGCTCCA GACCACGACA AGTGGGTTAGA GACCGTCAAG GAACTCATGA AGGCTGTTGA 300

CGAGTACATC CCAACCCCAA CTCACGATCT TGACAAGCCA TTCTTGATGC CAATCGAAGA 360
TGTGTTTACC ATCTCCGGTC GTGGTYCCGT TGTCACCGGT CGTGTTGAGC GTGGTAAGCT 420
CCCAATCAAC ACCCCAGTTG AGATCGTTGG TTTGCGCGAT ACCCAGACCA CCACCGTCAC 480
CTCTATCGAG ACCTTCCACA AGCAGATGGA TGAGGCAGAG GCTGGCGATA ACACTGGTCT 540
TCTTCTCCGC GGTATCAACC GTACCGACGT TGAGCGTGGT CAGGTTGTGG CTGCTCCAGG 600
TTCTGTGACT CCACACACCA AGTTCGAAGG CGAAGTTTAC GTCTTGACCA AGGACGAAGG 660
TGGCCGTCAC TCGCCATTCT TCTCCAATA CCGTCCACAG TTCTACTTCC GTACCACCGA 720
TGTTACTGGC GTTATCACCT TGCCAGACGG CATCGAAATG GTTCAGCCAG GCGATCACGC 780
AACCTTCACT GTTGAGTTGA TCCAGGCTAT CGCAATGGAA GAG 823

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria innocua*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAACTC GTGAACATAT 60
CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT 120
GGTTGACGAT GAAGAATTAC TAGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA 180
ATATGAATTC CCTGGCGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA 240
AGGTGAAGCT GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT 300
TCCAACCTCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC 360
AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGTGAA CGTGGACAAG TTAAAGTTGG 420
TGACGAAGTA GAAGTTATCG GTATTGAAGA AGAAAGCAAA AAAGTAGTAG TAACTGGAGT 480
AGAAATGTTT CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT 540
ACGTGGTGTT GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTAGCTAAAC CAGGTTTCAT 600
TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG AAGGTGGACG 660
TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC 720

TGGTATTGTT ACACTTCCAG AAGGTACTGA AATGGTAATG CCTGGTGATA ACATTGAGCT 780
TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC 817

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria ivanovii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC GTGAACATAT 60
TCTTACTTTC ACGTCAAGTT GGTGTTCCAT ACATCGTTGT ATTCATGAAC AAATGTGACA 120
TGGTTGACGA TGAAGAATTA CTTGAATTAG TTGAAATGGA AATTCGTGAT CTATTAAGT 180
AATATGAATT CCCTGGCGAC GACATTCCTG TAATCAAAGG TTCAGCTCTT AAAGCACTTC 240
AAGGTGAAGC TGATTGGGAA GCTAAAATTG ACGAGTTAAT GGAAGCTGTA GATTCTTACA 300
TTCCAAGTCC AGAACGTGAT ACTGACAAAC CATTATGAT GCCAGTTGAG GATGTATTCT 360
CAATCACTGG TCGTGGAACA GTTGCAACTG GACGTGTTGA ACGTGGACAA GTTAAAGTTG 420
GTGACGAAGT AGAAGTTATC GGTATTGAAG AAGAAAGCAA AAAAGTAGTA GTAAGTGGAG 480
TAGAAATGTT CCGTAAATTA CTAGACTACG CTGAAGCTGG CGACAACATT GGCGCACTTC 540
TACGTGGTGT TGCTCGTGAA GATATCCAAC GTGGTCAAGT ATTAGCTAAA CCAGGTTCGA 600
TTACTCCACA TACTAACTTC AAAGCTGAAA CTTATGTTTT AACTAAAGAA GAAGGTGGAC 660
GTCATACTCC ATTCTTCAAC AACTACCGCC CACAATTCTA TTTCCGTACT ACTGACGTAA 720
CTGGTATTGT TACACTTCCA GAAGGTACTG AAATGGTAAT GCCTGGTGAT AACATTGAGC 780
TTGCAGTTGA ACTAATTGCA CCAATCGCTA TCGAAGAC 818

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACATAT 60
CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT 120
GGTTGACGAT GAAGAATTAC TAGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA 180
ATATGAATTC CCTGGCGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA 240
AGGTGAAGCT GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT 300
TCCAACCTCCW GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC 360
AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGTTGAA CGTGGAACAAG TTAAAGTTGG 420
TGACGAAGTA GAAGTTATCG GTATCGAAGA AGAAAGCAAA AAAGTAGTAG TAACTGGAGT 480
AGAAATGTTT CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT 540
ACGTGGTGTT GCTCGTGAAG ATATCCAACR TGGTCAAGTA TTAGCTAAAC CAGGTTTCGAT 600
TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG AAGGTGGACG 660
TCACACTCCA TTCTTCAACA ACTACGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC 720
TGGTATTGTT ACACTTCCAG AAGGTACTGA AATGGTAAYG CCTGGTGATA ACATTGAGCT 780
TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC 817

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria seeligeri*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACATAT 60
CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT 120
GGTTGACGAT GAAGAATTAC TTGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA 180
ATATGAATTC CCTGGTGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA 240

AGGTGAAGCT GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT	300
TCCAACCTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC	360
AATCACTGGT CGTGGAACTG TTGCAACTGG ACGTGTGAA CGTGGACAAG TTAAAGTTGG	420
TGACGAAGTA GAAGTTATCG GTATTGAAGA AGAAAGCAAA AAAGTAATAG TAACTGGAGT	480
AGAAATGTTC CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT	540
ACGTGGTGTT GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTAGCTAAAC CAGGTTCGAT	600
TACTCCACAT ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAGAAG AAGGTGGACG	660
TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC	720
TGGTATTGTT ACACTTCCAG AAGGTACTGA AATGGTAATG CCTGGTGATA ACATTGAGCT	780
TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC	817

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

CGGTGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCACAACTC GTGAACACAT	60
TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA TTCTTAAACA AAGTTGACAT	120
GGTTGACGAT GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTAAGCGA	180
ATATGACTTC CCAGGTGACG ATGTACCTGT AATCGCTGGT TCAGCATTAR AAGCTTTAGA	240
AGGCGATGCT CAATACGAAG AAAAAATCTT AGAATTARTG GAAGCTGTAG ATACTTACAT	300
TCCAACCTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC	360
AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA CGTGGTCAA TCAAAGTTGG	420
TGAAGAAGTT GAAATCATCG GTTTACATGA CACATCTAAA ACAACTGTTA CAGGTGTTGA	480
AATGTTCCGT AAATTATTAG ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG	540
TGGTGTGCT CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC	600
ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG GTGGACGTCA	660

CACTCCATTC TTCTCAAAC ATCGTCCACA ATTCTATTTTC CGTACTACTG ACGTAACTGG 720
TGTTGTTTAC TTACCAGAAG GTACTGAAAT GGTAATGCCT GGTGATAACG TTGAAATGAC 780
AGTAGAATTA ATCGCTCCAA TCGCGATTGA AGAC 814

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

CGGCGGTATC TTAGTTGTAT CTGCTGCTGA CGGTCCAATG CCACAACTC GTGAACACAT 60
CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA TTCTTAAACA AAGTTGACAT 120
GGTAGACGAC GAAGAATTAT TAGAATTAGT TGAAATGGAA GTTCGTGACT TATTAAGCGA 180
ATATGACTTC CCAGGTGACG ATGTACCTGT AATCGCTGGT TCTGCATTAA AAGCATTAGA 240
AGGCGATGCT GAATACGAAC AAAAAATCTT AGACTTAATG CAAGCAGTTG ATGATTACAT 300
TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC 360
AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA CGTGGTCAAA TCAAAGTWGG 420
TGAAGAAGTT GAAATCATCG GTATGCACGA AACTTCTAAA ACAACTGTTA CTGGTGTAGA 480
AATGTTCCGT AAATTATTAG ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG 540
TGGTGTGCA CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCTATTAC 600
ACCACACACA AAATTCAAAG CTGAAGTATA CGTATTATCT AAAGATGAAG GTGGACGTCA 660
CACTCCATTC TTCCTAACT ATCGCCCA ATCTATTTTC CRTACTACTG ACGTAACTGG 720
TGTTGTAAAC TTACCAGAAG GTACAGAAAT GGTATGCCT GGCGACAACG TTGAAATGAC 780
AGTTGAATTA ATCGCTCCAA TCGCTATCGA AGAC 814

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

09989643 1300

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACACAT 60
TCTTTTATCA CGTRACGTTG GTGYTCCAGC ATTAGTTGTA TTCTTAAACA AAGTTGACAT 120
GGTTGACGAY GAAGAATTAT TAGAATTRGT AGAAATGGAA GTTCGTGRCT TATTAAGCGA 180
ATATGACTTC CCAGGTGACG ATGTACCTGT AATCTCTGGT TCTGCATTAA AAGCTTTAGA 240
AGGCGACGCT GACTATGAGC AAAAAATCTT AGACTTAATG CAAGCTGTTG ATGACTYCAT 300
TCCAACACCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC 360
AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA CGTGGTCAAA TCAAAGTCGG 420
TGAAGAAATC GARATCATCG GTATGCAAGA AGAATCAAGC AAAACAACTG TTACTGGTGT 480
AGAAATGTTC CGTAAATTAT TAGACTACGC TGAAGCTGGT GACAACATTG GTGCATTATT 540
ACGTGGTGTT TCACGTGATG ATGTACAACG TGGTCAAGTT TTAGCTGCTC CTGGTACTAT 600
CACACCACAT ACAAATTC AAGCGGATGT TTACGTTTTA TCTAAAGATG AAGGTGGTCG 660
TCATACGCCA TTCTTCACTA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC 720
TGGTGTGTT AACTTACCAG AAGGTACTGA AATGGTTATG CCTGGCGATA ACGTTGAAAT 780
GGATGTTGAA TTAATTTCTC CAATCGCTAT TGAAGAC 817

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 817 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus simulans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

CGGCGGTATC TTAGTAGTAT CTGCTGCAGA TGGTCCAATG CCACAAACTC GTGAACACAT 60
CTTATTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA TTCTTAAACA AAGCTGACAT 120
GGTTGACGAC GAAGAATTAT TAGAATTAGT TGAAATGGAA GTTCGTGACT TATTATCTGA 180

ATACGACTTC CCTGGTGACG ATGTACCAGT TATCGTTGGT TCTGCATTAA AAGCTTTAGA 240
 AGGCGACCCA GAATACGAAC AAAAAATCTT AGACTTAATG CAAGCTGTAG ATGACTACAT 300
 CCCAACTCCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC 360
 AATCACTGGT CGTGGTACTG TAGCAACAGG CCGTGTGAA CGTGGTCAAA TCAAAGTCGG 420
 TGAAGAAGTT GAAATCATCG GTATCACTGA AGAAAGCAAG AAAACAACAG TTACAGGTGT 480
 AGAAATGTTT CGTAAATTAT TAGACTACGC TGAAGCTGGT GACAACATCG GTGCTTTATT 540
 ACGTGGTGTT GCACGTGAAG ACGTACAACG TGGACAAGTA TTAGCAGCTC CTGGCTCTAT 600
 TACTCCACAC AAAAAATTCA AAGCTGATGT TTACGTTTTA TCTAAAGAAG AAGGTGGACG 660
 TCATACTCCA TTCTTCACTA ACTACCGCCC ACAATTCTAC TTCCGTACTA CTGACGTAAC 720
 TGGCGTTGTT CACTTACCAG AAGGTACTGA AATGGTTATG CCTGGCGATA ACGTAGAAAT 780
 GACTGTTGAA TTGATCGCTC CAATCGCGAT TGAAGAC 817

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

CGGAGCTATC CTTGTAGTTG CTTCAACTGA TGGACCAATG CCACAAACTC GTGAGCACAT 60
 CCTTCTTTCA CGTCAAGTTG GTGTTAAACA CCTTATCGTA TTCATGAACA AAGTTGACCT 120
 TGTTGATGAT GAAGAATTGC TTGAATTGGT TGAAATGGAA ATTCGTGACC TTCTTTCAGA 180
 ATACGACTTC CCAGGTGATG ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCACTTGA 240
 AGGCGACGAA AAATACGAAG ACATCATCAT GGAATTGATG AGCACTGTTG ATGAGTACAT 300
 TCCAGAACCA GAACGTGATA CTGACAAACC TTTACTTCTT CCAGTTGAAG ATGTATTCTC 360
 AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC CGTGGTACTG TTCGTGTCAA 420
 CGACGAAGTT GAAATCGTTG GTATTAAAGA AGATATCCAA AAAGCAGTTG TTACTGGTGT 480
 TGAAATGTTT CGTAAACAAC TTGACGAAGG TCTTGCAAGG GACAACGTTG GTGTTCTTCT 540
 TCGTGGTGTT CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT 600

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CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT TCTAAAGAAG AAGGTGGACG	660
TCATACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC TTCCGTACAA CTGACGTAAC	720
AGGTTCAATC GAACTTCCAG CAGGAACAGA AATGGTTATG CCTGGTGATA ACGTTACTAT	780
CGAAGTTGAA TTGATTCACC CAATCGCCGT AGAACAA	817

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

CGGAGCTATC CTTGTAGTAG CTTCAACTGA CGGACCAATG CCACAAACTC GTGAGCACAT	60
CCTTCTTTCA CGTCAGGTTG GTGTAAACA CCTTATCGTC TTCATGAACA AAGTTGACTT	120
GGTTGACGAC GAAGAATTGC TTGAATTGGT TGAAATGGAA ATCCGTGACC TATTGTCAGA	180
ATACGACTTC CCAGGTGACG ATCTTCCAGT TATCCAAGGT TCAGCACTTA AAGCTCTTGA	240
AGGTGACTCT AAATACGAAG ACATCGTTAT GGAATTGATG AACACAGTTG ATGAGTATAT	300
CCCAGAACCA GAACGTGACA CTGACAAACC ATTGCTTCTT CCAGTCGAGG ACGTATTCTC	360
AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC CGTGGTATCG TTAAAGTCAA	420
CGACGAAATC GAAATCGTTG GTATCAAAGA AGAACTCRA AAAGCAGTTG TTACTGGTGT	480
TGAAATGTTT CGTAAACAAC TTGACGAAGG TCTTGCTGGA GATAACGTAG GTGTCCTTCT	540
TCGTGGTGTT CAACGTGATG AAATCGAACG TGGACAAGTT ATCGCTAAAC CAGGTTCAAT	600
CAACCCACAC ACTAAATTCA AAGGTGAAGT CTACATCCTT ACTAAAGAAG AAGGTGGACG	660
TCACACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC TTCCGTACTA CTGACGTTAC	720
AGGTTCAATC GAACTTCCAG CAGGTACTGA AATGGTAATG CCTGGTGATA ACGTGACAAT	780
CGACGTTGAG TTGATTCACC CAATCGCCGT AGAACAA	817

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus salivarius*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

CGGTGCGATC CTTGTAGTAG CATCTACTGA CGGACCAATG CCACAAACTC GTGAGCACAT	60
CCTTCTTTCA CGTCAGGTTG GTGTAAACA CCTTATCGTC TTCATGAACA AAGTTGACTT	120
GGTTGACGAT GAAGAATTGC TTGAATTGGT TGAAATGGAA ATCCGTGACC TTCTTTCAGA	180
ATACGATTTC CCAGGTGATG ACATTCCAGT TATCCAAGGT TCAGCTCTTA AAGCTCTTGA	240
AGGTGATTCT AAATACGAAG ACATCATCAT GGACTTGATG AACACTGTTG ACGAATACAT	300
CCCAGAACCA GAACGTGACA CTGACAAACC ATTGTTGCTT CCAGTCGAAG ACGTATTCTC	360
AATCACTGGT CGTGGTACTG TTGCTTCAGG ACGTATCGAC CGTGGTGTTG TTCGTGTCAA	420
TGACGAAGTT GAAATCGTTG GTCTTAAAGA AGACATCCAA AAAGCAGTTG TTACTGGTGT	480
TGAAATGTTT CGTAAACAAC TTGACGRAGG TATTGCCGGA GATAACGTCG GTGTTCTTCT	540
TCGTGGTATC CAACGTGATG AAATCGAACG TGGTCAAGTA TTGGCTGCAC CTGGTTCAAT	600
CAACCCACAC ACTAAATTCA AAGGTGAAGT TTACATCCTT TCTAAAGAAG AAGGTGGACG	660
TCACACTCCA TTCTTCAACA ACTACCGTCC ACAGTTCTAC TTCCGTACAA CTGACGTAAC	720
AGGTTCAATC GAACTTCCTG CAGGTACTGA AATGGTTATG CCTGGTGATA ACGTGAATAT	780
CGACGTTGAG TTGATCCACC CAATCGCCGT TGAACAA	817

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Agrobacterium tumefaciens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

AACATGATCA CCGGTGCTGC CGAGATGGAC GGCGCGATCC TGGTTTGCTC GGCTGCCGAC	60
GGCCCGATGC CACAGACCCG CGAGCACATC CTGCTTGCCC GTCAGGTGGG CGTTCGGGCC	120

ATCGTCGTGT TCCTCAACAA GGTGACGACCAG GTTGACGACG CCGAGCTTCT CGAGCTCGTC 180
 GAGCTTGAAG TTCGCGAACT TCTGTGCTCC TACGACTTCC CGGGCGACGA TATCCCGATC 240
 ATCAAGGGTT CGGCACTTGC TGCTCTTGAA GATTCTGACA AGAAGATCGG TGAAGACGCG 300
 ATCCGCGAGC TGATGGCTGC TGTCGACGCC TACATCCCGA CGCCTGAGCG TCCGATCGAC 360
 CAGCCGTTCC TGATGCCGAT CGAAGACGTG TTCTCGATCT CGGGTCGTGG TACGGTTGTG 420
 ACGGGTCGCG TTGAGCGCGG TATCGTCAAG GTTGGTGAAG AAGTCGAAAT CGTCGGCATC 480
 CGTCCGACCT CGAAGACGAC TGTTACCGGC GTTGAAATGT TCCGCAAGCT GCTCGACCAG 540
 GGCCAGGCCG GCGACAACAT CCGTGCACTC GTTCGCGGCG TTACCCGTGA CGGCGTCGAG 600
 CGTGGTCAGA TCCTGTGCAA GCCGGGTTTCG GTCAAGCCGC ACAAGAAGTT CATGGCAGAA 660
 GCCTACATCC TGACGAAGGA AGAAGGCGGC CGTCATACGC CGTTCTTCAC GAACTACCGT 720
 CCGCAGTTCT ACTTCCGTAC GACTGACGTT ACCGGTATCG TTTCGCTTCC TGAAGGCACG 780
 GAAATGGTTA TGCCTGGCGA CAACGTCCT GTTGAAGTCG AGCTGATCGT TCCGATCGCG 840
 ATGGAAGAAA AGCTGCGCTT CGCTATCCGC GAAGGCGGCC GTACCGTCGG CGCCGGC 897

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus subtilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

ATGATCACTG GTGCTGCGCA AATGGACGGA GCTATCCTTG TAGTATCTGC TGCTGATGGC 60
 CCAATGCCAC AAACCTCGTGA GCACATCCTT CTTTCTAAAA ACGTTGGTGT ACCATACATC 120
 GTTGTATTCT TAAACAAATG CGACATGGTA GACGACGAAG AGCTTCTTGA ACTAGTTGAA 180
 ATGGAAGTTC GCGATCTTCT TAGCGAATAC GACTTCCCTG GTGATGATGT ACCAGTTGTT 240
 AAAGGTTCTG CTCTTAAAGC TCTTGAAGGA GACGCTGAGT GGGAAGCTAA AATCTTCGAA 300
 CTTATGGATG CGGTTGATGA GTACATCCCA ACTCCAGAAC GCGACACTGA AAAACCATTC 360
 ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACAGTTGC TACTGGCCGT 420
 GTAGAACGCG GACAAGTTAA AGTCGGTGAC GAAGTTGAAA TCATCGGTCT TCAAGAAGAG 480

AACAAGAAAA CAACTGTTAC AGGTGTTGAA ATGTTCCGTA AGCTTCTTGA TTACGCTGAA 540
GCTGGTGACA ACATTGGTGC CCTTCTTCGC GGTGTATCTC GTGAAGAAAT CCAACGTGGT 600
CAAGTACTTG CTAAACCAGG TACAATCACT CCACACAGCA AATTCAAAGC TGAAGTTTAC 660
GTTCTTTCTA AAGAAGAGGG TGGACGTCAT ACTCCATTCT TCTCTAACTA CCGTCCTCAG 720
TTCTACTTCC GTACAACTGA CGTAACTGGT ATCATCCATC TTCCAGAAGG CGTAGAAATG 780
GTTATGCCTG GAGATAACAC TGAAATGAAC GTTGAACCTA TTTCTACAAT CGCTATCGAA 840
GAAGGAACTC GTTTCTCTAT TCGTGAAGGC GGACGTACTG TTGGT 885

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides fragilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

ATGGTTACTG GTGCTGCTCA GATGGACGGT GCTATCATTG TAGTTGCTGC TACTGATGGT 60
CCGATGCCTC AGACTCGTGA GCACATCCTT TTGGCTCGTC AGGTAAACGT TCCGAAGCTG 120
GTTGTATTCA TGAACAAGTG CGATATGGTT GAAGATGCTG AGATGTTGGA ACTTGTTGAA 180
ATGGAAATGA GAGAATTGCT TTCATTCTAT GATTTCGACG GTGACAATAC TCCGATCATT 240
CAGGGTTCTG CTCTTGGTGC ATTGAACGGC GTAGAAAAAT GGGAAGACAA AGTAATGGAA 300
CTGATGGAAG CTGTTGATAC TTGGATTCCA CTGCCTCCGC GCGATGTTGA TAAACCTTTC 360
TTGATGCCGG TAGAAGACGT GTTCTCTATC ACAGGTCGTG GTACTGTAGC TACAGGTCGT 420
ATCGAAACTG GTGTTATCCA TGTAGGTGAT GAAATCGAAA TCCTCGGTTT GGGTGAAGAT 480
AAGAAATCAG TTGTAACAGG TGTGAAATG TTCCGCAAAC TTCTGGATCA GGGTGAAGCT 540
GGTGACAACG TAGGTCTGTT GCTTCGTGGT GTTGACAAGA ACGAAATCAA ACGTGGTATG 600
GTTCTTTGTA AACCAGGTCA GATTAAACCT CACTCTAAAT TCAAAGCAGA GGTTTATATC 660
CTGAAGAAAG AAGAAGGTGG TCGTCACACT CCATTCCATA ACAAATATCG TCCTCAGTTC 720
TACCTGCGTA CTATGGACTG TACAGGTGAA ATCACTCTTC CGGAAGGAAC TGAAATGGTA 780
ATGCCGGGTG ATAACGTAAC TATCACTGTA GAGTTGATCT ATCCGGTTGC ACTGAACATC 840

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GGTCTTCGTT TCGCTATCCG CGAAGGTGGA CGTACAGTAG GT

882

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

AATATGATTA CAGGAGCAGC TCAAATGGAT GCAGCGATAC TTTTAGTTGC TGCTGATAGT 60
GGTGCTGAGC CTCAAACAAA AGAGCATTTG CTTCTTGCTC AAAGAATGGG AATAAAGAAA 120
ATAATAGTTT TTTTAAATAA ATTGGACTTA GCAGATCCTG AACTTGTTGA GCTTGTTGAA 180
GTTGAAGTTT TAGAACTTGT TGAAAAATAT GGCTTTTCAG CTGATACTCC AATAATCAAA 240
GGTTCAGCTT TTGGGGCTAT GTCAAATCCA GAAGATCCTG AATCTACAAA ATGCGTTAAA 300
GAACTTCTTG AATCTATGGA TAATTATTTT GATCTTCAG AAAGAGATAT TGACAAGCCA 360
TTTTTGCTTG CTGTTGAAGA TGTATTTTCT ATTTCAGGAA GAGGCACTGT TGCTACTGGG 420
CGTATTGAAA GAGGTATTAT TAAAGTTGGT CAAGAAGTTG AAATAGTTGG AATTAAAGAA 480
ACCAGAAAAA CTA CTGTTAC TGGTGTGAA ATGTTCCAGA AAATTCTTGA GCAAGGTCAA 540
GCAGGGGATA ATGTTGGTCT TCTTTTGAGA GGC GTTGATA AAAAAGACAT TGAGAGGGGG 600
CAAGTTTTGT CAGCTCCAGG TACAATTACT CCACACAAGA AATTTAAAGC TTCAATTTAT 660
TGTTTGACTA AAGAAGAAGG CGGTAGGCAC AAGCCATTTT TCCAGGGTA TAGACCACAG 720
TTCTTTTTTA GAACAACCGA TGTTACTGGA GTTGTTGCTT TAGAGGGCAA AGAAATGGTT 780
ATGCCTGGTG ATAATGTTGA TATTATTGTT GAGCTGATCT CTTCAATAGC TATGGATAAG 840
AATGTAGAAT TTGCTGTTCT AGAAGGTGGA AGAACCGTTG CTT CAGGA 888

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

09569543 13001

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Brevibacterium linens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

AACATGATCA CCGGTGCCGC TCAGATGGAC GGTGCGATCC TCGTCGTCGC CGCTACCGAC	60
GGACCGATGC CCCAGACCCG TGAGCACGTG CTGCTCGCGC GTCAGGTCGG CGTTCCCTAC	120
ATCGTCGTGG CTCTGAACAA GTCCGACATG GTCGATGACG AGGAGCTCCT CGAGCTCGTC	180
GAATTCGAGG TCCGCGACCT GCTCTCGAGC CAGGACTTCG ACGGAGACAA CGCTCCGGTC	240
ATTCCGGTGT CCGCTCTCAA GGCCTGGAA GGCAGCAGA AGTGGGTCAA GAGCGTTCAG	300
GATCTCATGG CTGCCGTCGA TGACAACGTT CCGGAGCCGG AGCGCGATGT CGACAAGCCG	360
TTCCTCATGC CCGTCGAGGA CGTCTTCACG ATCACC GGTC GTGGAACCGT CGTCACCGGT	420
CGTGTCGAGC GCGGCGTGCT CCTGCCTAAC GACGAAATCG AAATCGTCGG CATCAAGGAG	480
AAGTCGTCCA AGACGACTGT CACCGCTATC GAGATGTTCC GCAAGACCCT GCCGGATGCC	540
CGTGCAGGTG AGAACGTCGG TCTGCTCCTC CGCGGCACCA AGCGCGAGGA TGTTGAGCGC	600
GGTCAGGTCA TCGTGAAGCC GGGTTCGATC ACCCGCACCA CCAAGTTCGA GGCTCAGGTC	660
TACATCCTGA GCAAGGACGA GGGCGGACGT CACAACCCGT TCTACTCGAA CTACCGTCCG	720
CAGTTCTACT TCCGGACCAC GGACGTCACC GGTGTCATCA CGCTGCCCCGA GGGCACCGAG	780
ATGGTCATGC CCGGCGACAA CACCGATATG TCGGTCGAGC TCATCCAGCC GATCGCTATG	840
GAGGACCGCC TCCGCTTCGC AATCCGCGAA GGTGGCCGCA CCGTCGGCGC CCGT	894

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Burkholderia cepacia*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

ATGATCACGG GCGCAGCGCA GATGGACGGC GCGATCCTGG TTTGCTCGGC AGCAGACGGC	60
CCGATGCCGC AAACGCGTGA GCACATCCTG CTGGCGCGTC AGGTTGGTGT TCCGTACATC	120
ATCGTGTTC TGAACAAGTG CGACAGTGTG GACGACGCTG AACTGCTCGA GCTGGTCGAG	180

ATGGAAGTTC GCGAACTCCT GTCGAAGTAC GACTTCCCGG GCGACGACAC GCCGATCGTG 240
AAGGGTTTCGG CCAAGCTGGC GCTGGAAGGC GACACGGGCG AGCTGGGCGA AGTGGCGATC 300
ATGAGCCTGG CAGACGCGCT GGACACGTAC ATCCCGACGC CGGAGCGTGC AGTTGACGGC 360
GCGTTCCTGA TGCCGGTGGA AGACGTGTTT TCGATCTCGG GCCGTGGTAC GGTGGTGACG 420
GGTCGTGTCTG AGCGCGGCAT CGTGAAGGTC GGC GAAGAAA TCGAAATCGT CGGTATCAAG 480
CCGACGGTGA AGACGACCTG CACGGGCGTT GAAATGTTCC GCAAGCTGCT GGACCAAGGT 540
CAGGCAGGCG ACAACGTCGG TATCCTGCTG CGCGGCACGA AGCGTGAAGA CGTGGAGCGT 600
GGCCAGGTTC TGGCGAAGCC GGGTTCGATC ACGCCGCACA CGCACTTCAC GGCTGAAGTG 660
TACGTGCTGA GCAAGGACGA AGGCGGCCGT CACACGCCGT TCTTCAACAA CTACCGTCCG 720
CAGTTCTACT TCCGTACGAC GGACGTGACG GGCTCGATCG AGCTGCCGAA GGACAAGGAA 780
ATGGTGATGC CGGGCGACAA CGTGTCGATC ACGGTGAAGC TGATTGCTCC GATCGCGATG 840
GAAGAAGGTC TGCGCTTCGC AATCCGTGAA GGCGGCCGTA CGGTCGGC 888

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia trachomatis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

AACATGATCA CCGGTGCGGC TCAAATGGAC GGGGCTATTC TAGTAGTTTC TGCAACAGAC 60
GGAGCTATGC CTCAAATAA AGAGCATATT CTTTGGCAA GACAAGTTGG GGTTCCTTAC 120
ATCGTTGTTT TTCTCAATAA AATTGACATG ATTTCCGAAG AAGACGCTGA ATTGGTCGAC 180
TTGGTTGAGA TGGAGTTGGC TGAGCTTCTT GAAGAGAAAAG GATACAAAGG GTGTCCAATC 240
ATCAGAGGTT CTGCTCTGAA AGCTTTGGAA GGAGATGCTG CATACATAGA GAAAGTTCTGA 300
GAGCTAATGC AAGCCGTCGA TGATAATATC CCTACTCCAG AAAGAGAAAT TGACAAGCCT 360
TTCTTAATGC CTATTGAGGA CGTGTTCTCT ATCTCCGAC GAGGAACTGT AGTAACTGGA 420
CGTATTGAGC GTGGAATTGT TAAAGTTTCC GATAAAGTTC AGTTGGTCGG TCTTAGAGAT 480
ACTAAAGAAA CGATTGTTAC TGGGGTTGAA ATGTTTCAGAA AAGAACTCCC AGAAGGTCGT 540

GCAGGAGAGA ACGTTGGATT GTCCTCAGA GGTATTGGTA AGAACGATGT GGAAAGAGGA 600
 ATGGTTGTTT GCTTGCCAAA CAGTGTAA CCTCATACAC AGTTTAAGTG TGCTGTTTAC 660
 GTTCTGCAAA AAGAAGAAGG TGGACGACAT AAGCCTTTCT TCACAGGATA TAGACCTCAA 720
 TTCTTCTTCC GTACAACAGA CGTTACAGGT GTGGTAACTC TGCCTGAGGG AGTTGAGATG 780
 GTCATGCCTG GGGATAACGT TGAGTTTGAA GTGCAATTGA TTAGCCCTGT GGCTTTAGAA 840
 GAAGGTATGA GATTTGCGAT TCGTGAAGGT GGTCGTACAA TCGGTGCTGG A 891

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

AACATGATCA CCGGTGCTGC GCAGATGGAC GGCGCGATCC TGGTAGTTGC TGCGACTGAC 60
 GGCCCGATGC CGCAGACTCG TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC 120
 ATCATCGTGT TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 180
 GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC 240
 GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC GAAAATCCTG 300
 GAACTGGCTG GCTTCCTGGA TTCTTACATT CCGGAACCAG AGCGTGCGAT TGACAAGCCG 360
 TTCCTGCTGC CGATCGAAGA CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT 420
 CGTGTAAGAC GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG 480
 ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT 540
 GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT CGAAGCTGGT 600
 CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA AGTTCGAATC TGAAGTGTAC 660
 ATTCTGTCCA AAGATGAAGG CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG 720
 TTCTACTTCC GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG 780
 GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCGATGGAC 840
 GACGGTCTGC GTTTCGCAAT CCGTGAAGGC GGCCGTACCG TTGGCGCGGG C 891

CCCTTCTTCC

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fibrobacter succinogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

AACATGGTGA CTGGTGCTGC TCAGATGGAC GCGCTATCC TCGTTGTTGC CGCTACTGAC 60
GGTCCGATGC CGCAGACTCG CGAACACATC CTTCTCGCTC ACCAGGTTGG CGTGCCGAAG 120
ATCGTCGTGT TCATGAACAA GTGCGACATG GTTGACGATG CTGAAATTCT CGACCTCGTC 180
GAAATGGAAG TTCGCGAACT CCTCTCCAAG TATGACTTCG ACGGTGACAA CACCCCGATC 240
ATCCGTGGTT CCGCTCTCAA GGCCCTCGAA GCGGATCCGG AATACCAGGA CAAGGTCATG 300
GAACTCATGA ACGCTTGCGA CGAATACATC CCGCTCCCGC AGCGCGATAC CGACAAGCCG 360
TTCCTCATGC CGATCGAAGA CGTGTTACAG ATTACTGGCC GCGGCACTGT CGCTACTGGC 420
CGTATCGAAC GCGGTGTCGT TCGCTTGAAC GACAAGGTTG AACGTATCGG TCTCGGTGAA 480
ACCACCGAAT ACGTCATCAC CCGTGTGTA ATGTTCCGTA AGCTCCTCGA CGACGCTCAG 540
GCAGGTGACA ACGTTGGTCT CCTCCTCCGT GGTGCTGAAA AGAAGGACAT CGTCCGTGGC 600
ATGGTTCTCG CAGCTCCGAA GTCTGTCACT CCGCACACCG AATTTAAGGC TGAAATCTAC 660
GTTCTCACGA AGGACGAAGG TGGCCGTCAC ACGCCGTTCA TGAATGGCTA CCGTCCGCAG 720
TTCTACTTCC GCACCACCGA CGTTACTGGT ACGATCCAGC TCCCGGAAGG TGTCGAAATG 780
GTTACTCCGG GTGACACGGT CACGATCCAC GTGAACCTCA TCGCTCCGAT CGCTATGGAA 840
AAGCAGCTCC GCTTCGCTAT CCGTGAAGGT GGACGTACTG TTGGTGCTGG C 891

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Flavobacterium ferrugineum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

AACATGATCA CCGGTGCTGC CCAGATGGAC GGTGCTATCT TAGTTGTGGC TGCATCAGAC 60
GGTCCTATGC CTCAAACAAA AGAACACATC CTGCTTGCTG CCCAGGTAGG TGTACCTAAA 120
ATGGTTGTGT TTCTGAATAA AGTTGACCTC GTTGACGACG AAGAGCTCCT GGAGCTGGTT 180
GAGATCGAGG TTCGCGAAGA ACTGACTAAA CGCGGTTTCG ACGGCGACAA CACTCCAATC 240
ATCAAAGGTT CCGCTACAGG CGCCCTCGCT GGTGAAGAAA AGTGGGTAA AGAAATTGAA 300
AACCTGATGG ACGCTGTTGA CAGCTACATC CCACTGCCTC CTCGTCCGGT TGATCTGCCG 360
TTCCTGATGA GCGTAGAGGA CGTATTCTCT ATCACTGGTC GTGGTACTGT TGCTACCGGT 420
CGTATCGAGC GTGGCCGTAT CAAAGTTGGT GAGCCTGTTG AGATCGTAGG TCTGCAGGAG 480
TCTCCCCTGA ACTCTACCGT TACAGGTGTT GAGATGTTCC GCAAACCTCT CGACGAAGGT 540
GAAGCTGGTG ATAACGCCGG TCTCCTCCTC CGTGGTGTG AAAAAACACA GATCCGTCGC 600
GGTATGGTAA TCGTTAAACC CGGTTCCATC ACTCCGCACA CGGACTTCAA AGGCGAAGTT 660
TACGTACTGA GCAAAGACGA AGGTGGCCGT CACACTCCAT TCTTCAACAA ATACCGTCCT 720
CAATTCTACT TCCGTACAAC TGACGTTACA GGTGAAGTAG AACTGAACGC AGGAACAGAA 780
ATGGTTATGC CTGGTGATAA CACCAACCTG ACCGTTAAAC TGATCCAACC GATCGCTATG 840
GAAAAAGGTC TGAAATTCGC GATCCGCGAA GGTGGCCGTA CCGTAGGTGC AGGA 894

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

AATATGATTA CTGGTGCGGC ACAAATGGAT GGTGCTATTT TAGTAGTAGC AGCAACAGAT 60
GGTCCTATGC CACAACTCG TGAACACATC TTATTAGGTC GCCAAGTAGG TGTTCCATAC 120
ATCATCGTAT TCTTAAACAA ATGCGACATG GTAGATGACG AAGAGTTATT AGAATTAGTC 180
GAAATGGAAG TTCGTGAACT TCTATCTCAA TATGACTTCC CAGGTGACGA TACACCAATC 240

(2) INFORMATION FOR SEO ID NO: 158:

(A) LENGTH: 906 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

AACATGATCA	CCGGTGC	GGC	GCAAA	TGGAC	GGAGCGATT	TGGTTGTTTC	TGCAGCTGAT	60
GGCCCTATGC	CTCAA	ACTAG	GGAGCATATC	TTATTGTCTC	GTCAAGTAGG	CGTGCCTCAC		120
ATCGTTGTTT	TCTTAAACAA	ACAAGACATG	GTAGATGACC	AAGAATTGTT	AGAACTTGTA			180
GAAATGGAAG	TGCGCGAATT	GTTGAGCGCG	TATGAATTTT	CTGGCGATGA	CACTCCTATC			240
GTAGCGGGTT	CAGCTTTAAG	AGCTTTAGAA	GAAGCAAAGG	CTGGTAATGT	GGGTGAATGG			300
GGTGAAAAAG	TGCTTAAACT	TATGGCTGAA	GTGGATGCCT	ATATCCCTAC	TCCAGAAAAG			360
GACACTGAAA	AAACTTTCTT	GATGCCGGTT	GAAGATGTGT	TCTCTATTGC	GGGTAGAGGG			420
ACTGTGGTTA	CAGGTAGGAT	TGAAAGAGGC	GTGGTGAAAG	TAGGCGATGA	AGTGGAATC			480
GTTGGTATCA	GACCTACACA	AAAAACGACT	GTAACCGGTG	TAGAAATGTT	TAGGAAAGAG			540
TTGGAAAAAG	GTGAAGCCGG	CGATAATGTG	GGCGTGCTTT	TGAGAGGAAC	TAAAAAAGAA			600

GAAGTGGAAC GCGGTATGGT TCTATGCAAA CCAGGTTCTA TCACTCCGCA CAAGAAATTT	660
GAGGGAGAAA TTTATGTCCT TTCTAAAGAA GAAGGCGGGA GACACACTCC ATTCTTCACC	720
AATTACCGCC CGCAATTCTA TGTGCGCACA ACTGATGTGA CTGGCTCTAT CACCCTTCCT	780
GAAGGCGTAG AAATGGTTAT GCCTGGCGAT AATGTGAAAA TCACTGTAGA GTTGATTAGC	840
CCTGTTGCGT TAGAGTTGGG AACTAAATTT GCGATTCGTG AAGGCGGTAG GACCGTTGGT	900
GCTGGT	906

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Micrococcus luteus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

AACATGATCA CCGGCGCCGC TCAGATGGAC GCGCGGATCC TCGTGGTCGC CGCTACCGAC	60
GGCCCGATGG CCCAGACCCG TGAGCACGTG CTCCTGGCCC GCCAGGTCGG CGTGCCGGCC	120
CTGCTCGTGG CCCTGAACAA GTCGGACATG GTGGAGGACG AGGAGCTCCT CGAGCGTGTC	180
GAGATGGAGG TCCGGCAGCT GCTGTCCTCC AGGAGCTTCG ACGTCGACGA GGCCCCGGTC	240
ATCCGCACCT CCGCTCTGAA GGCCCTCGAG GCGGACCCCC AGTGGGTCAA GTCCGTCGAG	300
GACCTCATGG ATGCCGTGGA CGAGTACATC CCGGACCCGG TCGCGGACAA GGACAAGCCG	360
TTCCTGATGC CGATCGAGGA CGTCTTCACG ATCACC GGCC GTGGCACC GTGACCGGT	420
CGCGCCGAGC GCGGCACCCT GAAGATCAAC TCCGAGGTCG AGATCGTCGG CATCCGCGAC	480
GTGCAGAAGA CCACTGTCAC CGGCATCGAG ATGTTCCACA AGCAGCTCGA CGAGGCCTGG	540
GCCGGCGAGA ACTGCGGTCT GCTCGTGCGC GGTCTGAAGC GCGACGACGT CGAGCGCGGC	600
CAGGTGCTGG TGGAGCCGGG CTCCATCACC CCGCACACCA ACTTCGAGGC GAACGTCTAC	660
ATCCTGTCCA AGGACGAGGG TGGGCGTCAC ACCCCGTTCT ACTCGAACTA CCGCGCGCAG	720
TTCTACTTCC GCACCACCGA CGTCACCGGC GTCATCACGC TGCCCGAGGG CACCGAGATG	780
GTCATGCCCC GCGACACCAC CGAGATGTCG GTCGAGCTCA TCCAGCCGAT CGCCATGGAG	840
GAGGGCCTCG GCTTCGCCAT CCGCGAGGGT GGCCGCACCG TGGGCTCCGG C	891

0909643-12001

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

AACATGATCA CCGGCGCCGC GCAGATGGAC GGTGCGATCC TGGTGGTCGC CGCCACCGAC 60
GGCCCGATGC CCCAGACCCG CGAGCACGTT CTGCTGGCGC GTCAAGTGGG TGTGCCCTAC 120
ATCCTGGTAG CGCTGAACAA GGCCGACGCA GTGGACGACG AGGAGCTGCT CGAACTCGTC 180
GAGATGGAGG TCCGCGAGCT GCTGGCTGCC CAGGAATTCG ACGAGGACGC CCCGGTTGTG 240
CGGGTCTCGG CGCTCAAGGC GCTCGAGGGT GACGCGAAGT GGGTTGCCTC TGTCGAGGAA 300
CTGATGAACG CGGTGACGA GTCGATTCCG GACCCGGTCC GCGAGACCGA CAAGCCGTTC 360
CTGATGCCGG TCGAGGACGT CTTCAACATT ACCGGCCGCG GAACCGTGGT CACCGGACGT 420
GTGGAGCGCG GCGTGATCAA CGTGAACGAG GAAGTTGAGA TCGTCGGCAT TCGCCCATCG 480
ACCACCAAGA CCACCGTCAC CGGTGTGGAG ATGTTCCGCA AGCTGCTCGA CCAGGGCCAG 540
GCGGGCGACA ACGTTGGTTT GCTGCTGCGG GGCCTCAAGC GCGAGGACGT CGAGCGTGGC 600
CAGGTTGTCA CCAAGCCCGG CACCACCACG CCGCACACCG AGTTCGAAGG CCAGGTCTAC 660
ATCCTGTCCA AGGACGAGGG CGGCCGGCAC ACGCCGTTCT TCAACAATA CCGTCCGCAG 720
TTCTACTTCC GCACCACCGA CGTGACCGGT GTGGTGACAC TGCCGGAGGG CACCGAGATG 780
GTGATGCCCG GTGACAACAC CAACATCTCG GTGAAGTTGA TCCAGCCCGT CGCCATGGAC 840
GAAGGTCTGC GTTTCGCGAT CCGCGAGGGT GGCCGCACCG TGGGCGCCGG C 891

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycoplasma genitalium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

AATATGATCA CAGGTGCTGC ACAAATGGAT GGAGCTATTC TAGTTGTTTC AGCAACTGAT 60
 AGTGTGATGC CCCAAACCCG CGAGCACATC TTAAGTGGCC GCCAAGTAGG GGTTCCTAAA 120
 ATGGTAGTTT TTCTAAACAA GTGTGATATT GCTAGTGATG AAGAGGTACA AGAACTTGTT 180
 GCTGAAGAAG TACGTGATCT GTTAACCTCC TATGGTTTTG ATGGTAAGAA CACTCCTATT 240
 ATTTATGGCT CAGCTTTAAA AGCATTGGAA GGTGATCCAA AGTGGGAGGC TAAGATCCAT 300
 GATTTGATTA AAGCAGTTGA TGAATGGATT CCAACTCCTA CACGTGAAGT AGATAAACCT 360
 TTCTTATTAG CAATTGAAGA TACGATGACC ATTACTGGTA GAGGTACAGT TGTTACAGGA 420
 AGAGTTGAAA GAGGTGAACT CAAAGTAGGT CAAGAAGTTG AAATTGTTGG TTAAAAACCA 480
 ATTAGAAAAG CAGTTGTTAC TGAATTTGAA ATGTTCAAAA AGGAACTTGA TTCAGCAATG 540
 GCTGGTGACA ATGCTGGGGT ATTATTACGT GGTGTTGAAC GTAAAGAAGT TGAAAGAGGT 600
 CAAGTTTTAG CAAAACCAGG CTCTATTAAA CCGCACAAGA AATTTAAAGC TGAGATCTAT 660
 GCTTTAAAGA AAGAAGAAGG TGGTAGACAC ACTGGTTTTT TAAACGGTTA CCGTCCTCAA 720
 TTCTATTTCC GTACCACTGA TGTAACGGT TCTATTGCTT TAGCTGAAAA TACTGAAATG 780
 GTTCTACCTG GTGATAATGC TTCTATTACT GTTGAGTTAA TTGCTCCTAT CGCTTGTGAA 840
 AAAGGTAGTA AGTTCTCAAT TCGTGAAGGT GGTAGAACTG TAGGGGCAGG C 891

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

AACATGATTA CCGGCGCCGC ACAAATGGAC GGTGCAATCC TGGTATGTTT TGCTGCCGAC 60
 GGCCCTATGC CGCAAACCCG CGAACACATC CTGCTGGCCC GTCAAGTAGG CGTACCTTAC 120
 ATCATCGTGT TCATGAACAA ATGCGACATG GTCGACGATG CCGAGCTGTT CCAACTGGTT 180
 GAAATGGAAA TCCGCGACCT GCTGTCCAGC TACGACTTCC CCGGCGACGA CTGCCCATC 240

(2) INFORMATION FOR SEO ID NO: 163:

(A) LENGTH: 891 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

AATATGATAA	CTGGTGCCGC	TCAGATGGAT	GGTGCTATAT	TAGTAGTTTC	TGCTGCTGAT	60
GGTCCTATGC	CTCAAAC TAG	AGAACATATA	TTACTGGCAA	AACAGGTAGG	TGTACCTGCT	120
ATGGTAGTAT	TTTTGAATAA	AGTAGATATG	G TAGATGATC	CTGACCTATT	AGAATTAGTT	180
GAGATGGAAG	TAAGAGAATT	ATTATCAAAA	TATGGTTTCC	CTGGTAATGA	AATACCTATT	240
ATTAAAGGTT	CTGCACTTCA	AGCTTTAGAA	GGAAAACCTG	AAGGTGAAAA	AGCTATTAAT	300
GAGTTAATGA	ATGCAGTAGA	TACGTATATA	CCTCAGCCTA	TAGAGCTACA	AGATAAACCT	360
TTTTTAATGC	CAATAGAGGA	TGTATTTTCT	ATTTCAGGCA	GAGGTACCGT	TGTA ACTGGT	420
AGAGTGGAGT	CAGGCATAAT	TAAGGTGGGT	GAAGAAATTG	AAATAGTAGG	TCTAAAAAAT	480
ACGCAAAAAA	C GACTTG TAC	AGGTGTAGAA	ATGTT CAGAA	AATTACTTGA	TGAAGGACAA	540
TCTGGAGATA	ATGTCGGTAT	ATTACTACGT	GGTACAAAAA	GAGAAGAAGT	AGAAAAGAGGA	600

(2) INFORMATION FOR SEQ ID NO: 164:

(A) LENGTH: 891 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella typhimurium*

AACATGATCA	CCGGTGCTGC	TCAGATGGAC	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	60
GGCCCCGATGC	CGCAGACCCG	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTC CGTAC	120
ATCATCGTGT	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAACTGGTT	180
GAGATGGAAG	TTCGCGAACT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	240
GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	GAAAAATCATC	300
GAACTGGCTG	GCTTCCTGGA	TTCTTATATT	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	360
TTCTTGCTGC	CGATCGAAGA	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	420
CGTGTAGAGC	GCGGTATCAT	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	480
ACTCAGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	540
GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	CGAACGTGGT	600
CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	660
ATTCTGTCCA	AAGATGAAGG	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	720
TTCTACTTCC	GTACTACTGA	CGTGACTGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	780
GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	CGCGATGGAC	840
GACGGTCTGC	GTTTCGCAAT	CCGTGAAGGC	GGCCGTACCG	TTGGCGCGGG	C	891

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 881 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putida*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

ATGATCACTG GTGCTGCACA GATGGACGGC GCGATTCTGG TAGTCGCTTC AACAGACGGT 60
CCAATGCCAC AGACTCGTGA GCACATCCTG CTTTCTCGTC AGGTTGGCGT ACCATTCATC 120
ATCGTATTCA TGAACAAATG TGACATGGTA GATGACGAAG AGCTGTTAGA GCTAGTTGAG 180
ATGGAAGTGC GTGAACTGTT ATCAGAATAC GATTTCCCAG GTGATGACTT ACCGGTAATC 240
CAAGGTTTCA CTCTGAAAGC GCTAGAAGGC GAGCCAGAGT GGAAGCAAA AATCCTTGAA 300
TTAGCAGCGG CGCTGGATTC TTACATTCCA GAACCACAAC GTGACATCGA TAAGCCGTTC 360
CTACTGCCAA TCGAAGACGT ATTCTCAATT TCAGGCCGTG GTACAGTAGT AACAGGTCGT 420
GTTGAGCGTG GTATTGTACG CGTAGGCGAC GAAGTTGAAA TCGTTGGTGT ACGTGCGACA 480
ACTAAGACAA CGTGTACTGG TGTAGAAATG TTCCGTAAAC TGCTTGACGA AGGTCGTGCA 540
GGTGAGAACT GTGGTATTTT GTTACGTGGT ACTAAGCGTG ATGACGTAGA ACGTGGTCAA 600
GTATTAGCGA AGCCAGGTTC AATCAACCCA CACACTACTT TTGAATCAGA AGTTTACGTA 660
CTGTCAAAAG AAGAAGGTGG TCGTCACACG CCATTCTTCA AAGGCTACCG TCCACAGTTC 720
TACTTCCGTA CAACTGACGT AACC GG TACT ATCGAACTGC CAGAAGGCGT AGAGATGGTA 780
ATGCCAGGCG ATAACATCAA GATGGTAGTG ACACTGATTT GCCCAATCGC GATGGACGAA 840
GGTTTACGCT TCGCAATCCG TGAAGGCGGT CGTACAGTGG T 881

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stigmatella aurantiaca*

09989643.12004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

AACATGATCA CGGGCGCGGC GCAGATGGAC GGAGCGATTC TGGTGGTGTC CGCGGCCGAC 60
GGCCCGATGC CCCAGACGCG TGAGCACATC CTGCTGGCCA GGCAGGTGGG CGTGCCCTAC 120
ATCGTCGTCT TCCTGAACAA GGTGGACATG CTGGACGATC CGGAGCTGCG CGAGCTGGTG 180
GAGATGGAGG TGCGCGACCT GCTCAAGAAG TACGAGTTCC CGGGCGACAG CATCCCCATC 240
ATCCCTGGCA GCGCGCTCAA GGCGCTGGAG GGAGACACCA GCGACATCGG CGAGGGAGCG 300
ATCCTGAAGC TGATGGCGGC GGTGGACGAG TACATCCCGA CGCCGACGCG TGCGACGGAC 360
AAGCCGTTCC TGATGCCGGT GGAAGACGTG TTCTCCATCG CAGGCCGAGG AACGGTGGCG 420
ACGGGCCGAG TGGAGCGCG CAAGATCAAG GTGGGCGAGG AAGTGGAGAT CGTGGGGATC 480
CGTCCGACGC AGAAGACGGT CATCACGGGG GTGGAGATGT TCCGCAAGCT GCTGGACGAG 540
GGCATGGCGG GAGACAACAT CGGAGCGCTG CTGCGAGGCC TGAAGCGCGA GGACCTGGAG 600
CGTGGGCAGG TGCTGGCGAA CTGGGGGAGC ATCAACCCGC ACACGAAGTT CAAGGCGCAG 660
GTGTACGTGC TGTCGAAGGA AGAGGGAGGG CGGCACACGC CGTTCTTCAA GGGATACCGG 720
CCGCAGTTCT ACTTCCGGAC GACGGACGTG ACCGGAACGG TGAAGCTGCC GGACAACGTG 780
GAGATGGTGA TGCCGGGAGA CAACATCGCC ATCGAGGTGG AGCTCATTAC TCCGGTCGCC 840
ATGGAGAAGG AGCTGCCGTT CGCCATCCGT GAGGGTGGCC GCACGGTGGG CGCCGGC 897

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

AACATGATCA CTGGTGCCGC TCAAATGGAC GGAGCTATCC TTGTAGTTGC TTCAACTGAT 60
GGACCAATGC CACAACTCG TGAGCACATC CTTCTTTCAC GTCAGGTTGG TGTAAACAC 120
CTTATCGTGT TCATGAACAA AGTTGACCTT GTTGATGACG AAGAGTTGCT TGAATTAGTT 180
GAGATGGAAA TTCGTGACCT TCTTTCAGAA TACGATTTC CAGGTGATGA CCTTCCAGTT 240
ATCCAAGGTT CAGCTCTTAA AGCTCTTGAA GGCGACACTA AATTTGAAGA CATCATCATG 300

GAATTGATGG ATACTGTTGA TTCATACATT CCAGAACCAG AACGCGACAC TGACAAACCA	360
TTGCTTCTTC CAGTCGAAGA CGTATTCTCA ATTACAGGTC GTGGTACAGT TGCTTCAGGA	420
CGTATCGACC GTGGTACTGT TCGTGTCAAC GACGAAATCG AAATCGTTGG TATCAAAGAA	480
GAAACTAAAA AAGCTGTTGT TACTGGTGTT GAAATGTTCC GTAAACAACT TGACGAAGGT	540
CTTGCAGGAG ACAACGTAGG TATCCTTCTT CGTGGTGTTT AACGTGACGA AATCGAACGT	600
GGTCAAGTTA TTGCTAAACC AAGTTCAATC AACCCACACA CTAAATTCAA AGGTGAAGTA	660
TATATCCTTT CTAAAGACGA AGGTGGACGT CACACTCCAT TCTTCAACAA CTACCGTCCA	720
CAATTCTACT TCCGTACAAC TGACGTAACA GGTTCATTCG AACTTCCAGC AGGTACAGAA	780
ATGGTTATGC CTGGTGATAA CGTGACAATC AACGTTGAGT TGATCCACCC AATCGCCGTA	840
GAACAAGGTA CTACTTTCTC AATCCGTGAA GGTGGACGTA CTGTTGGTTC AGGT	894

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Thiobacillus cuprinus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

AACATGATCA CCGGTGCGGC CCAGATGGAC GGCGCCATCC TGGTCGTGTC CGCCGCCGAC	60
GGCCCCATGC CCCAAACCCG CGAGCACATC CTGCTGGCGC GTCAGGTGGG CGTGCCCTAC	120
ATCATCGTGT TCCTCAACAA GTGCGACATG GTCGACGACG CCGAGCTGCT CGAACTCGTC	180
GAGATGGAAG TGCGCGAGCT GCTGTCCAAG TACGACTTCC CCGGTGACGA CACCCCCATC	240
ATCAAGGGCT CGGCCAAGCT GGCCCTCGAA GGCACAAAGG GCGAACTGGG CGAAGGCGCC	300
ATTCTCAAGC TGGCCGAGGC CCTGGACACC TACATCCCCA CGCCCGAGCG GGCCGTCGAC	360
GGCGCGTTCC TCATGCCCGT GGAAGACGTG TTCTCCATCT CCGGGCGCGG CACGGTGGTC	420
ACCGGGCGTG TGGAGCGCGG CATCATCAAG GTCGGCGAGG AAATCGAGAT TGTCGGCCTC	480
AAGCCCACCC TCAAGACCAC CTGCACCGGC GTGGAAATGT TCAGGAAGCT GCTCGACCAG	540
GGCCAGGCCG GCGACAACGT CGGCATCTTG CTGCGCGGCA CCAAGCGCGA GGAAGTCGAG	600
CGCGGCCAGG TGCTGTGCAA ACCCGGCTCG ATCAAGCCCC ACACCCACTT CACCGCCGAG	660

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GTGTACGTGC TGAGCAAGGA CGAGGGCGGC CGCCACACCC CCTTCTTCAA CAACTACCGC 720
CCGCAGTTCT ACTTCCGCAC CACCGACGTC ACCGGCGCCA TCGAACTGCC CAAGGACAAG 780
GAAATGGTCA TGCCCGGCGA TAATGTGAGC ATCACCGTCA AGCTCATCGC CCCCATCGCC 840
ATGGAAGAAG GCCTGCGCTT CGCCATCCGC GAAGGCGGCC GCACCGTCGG CGCCGGC 897

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Treponema pallidum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

AATATGATCA CGGGTGCTGC GCAGATGGAC GGTGGTATTC TCGTCGTGTC TGCGCCTGAC 60
GGCGTTATGC CACAGACGAA GGAGCATCTT CTGCTCGCCC GTCAGGTTGG TGTTCCTCC 120
ATCATTGTTT TTTTGAACAA GGTGATTTG GTTGATGATC CTGAGTTGCT AGAGCTGGTG 180
GAAGAAGAGG TCGGTGATGC GCTTGCTGGA TATGGGTTTT CGCGTGAGAC GCCTATCGTC 240
AAGGGGTCTG CGTTTAAAGC TCTGCAGGAT GGCGCTTCCC CGGAGGATGC AGCTTGATTT 300
GAGGAACTGC TTGCGGCCAT GGATTCCTAC TTTGAAGACC CAGTGCCTGA CGACGCAAGA 360
CCTTTCTTGC TCTCTATCGA GGATGTGTAC ACTATTTCTG GGCGTGGTAC CGTTGTCACG 420
GGGCGCATCG AATGTGGGGT AATTAGTCTG AATGAAGAGG TCGAGATCGT CGGGATTAAG 480
CCCACTAAGA AAACAGTGGT TACTGGCATT GAGATGTTTA ATAAGTTGCT TGATCAGGGA 540
ATTGCAGGTG ATAACGTGGG GCTGCTTTTG CGCGGGGTGG ATAAAAAAGA GGTGAGCGC 600
GGTCAGGTGC TTTCTAAGCC CGGTTCTATT AAGCCACACA CCAAGTTTGA GGCGCAGATC 660
TACGTGCTCT CTAAGGAAGA GGGTGCCGT CACAGTCCTT TTTTCAAGG TTATCGTCCG 720
CAGTTTTTATT TTAGAACTAC TGACATTACC GGTACGATTT CTCTTCCTGA AGGGGTAGAC 780
ATGGTGAAGC CGGGGGATAA CACCAAGATT ATAGGTGAGC TCATCCACCC GATAGCTATG 840
GACAAGGGTC TGAAGCTTGC GATTCGTGAA GGGGGGCGCA CTATTGCTTC TGGT 894

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

09985643 112001

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Ureaplasma urealyticum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

AATATGATTA CAGGGGCAGC ACAAATGGAT GGAGCAATTT TAGTTATTGC TGCATCTGAT 60
GGGGTTATGG CTCAAACATA AGAACATATT TTATTAGCAC GTCAAGTTGG TGTTCACAAA 120
ATCGTTGTTT TCTTAAACAA ATGTGATTTT ATGACAGATC CAGATATGCA AGATCTTGTT 180
GAAATGGAAG TTCGTGAATT ATTATCTAAA TATGGATTTG ATGGCGATAA CACACCAGTT 240
ATTCGTGGTT CAGGTCTTAA GGCTTTAGAA GGAGATCCAG TTTGAGAAGC AAAAATTGAT 300
GAATTAATGG ACGCAGTTGA TTCATGAATT CCATTACCAG AACGTAGTAC TGACAAACCA 360
TTCTTATTAG CAATTGAAGA TGTATTCACA ATTTCCAGGAC GTGGTACAGT AGTAACTGGA 420
CGTGTGAAC GTGGTGTATT AAAAGTTAAT GATGAGGTTG AAATTGTTGG TCTAAAAGAC 480
ACTCAAAAAA CTGTTGTTAC AGGAATTGAA ATGTTTAGAA AATCATTAGA TCAAGCTGAA 540
GCTGGTGATA ATGCTGGTAT TTTATTACGT GGTATTAAAA AAGAAGATGT TGAACGTGGT 600
CAAGTACTTG TAAAACCAGG ATCAATTAAA CCTCACCGTA CTTTTACTGC TAAAGTTTAT 660
ATTCTTAAAA AAGAAGAAGG TGGACGTCAT ACACCTATTG TTTCAGGATA CCGTCCACAA 720
TTCTATTTTA GAACAACAGA TGTAACAGGT GCTATTTTAT TACCTGCTGG TGTGATTGTT 780
GTTATGCCAG GTGATGACGT TGAAATGACT GTAGAATTAA TTGCTCCAGT TGCGATTGAA 840
GATGGATCTA AATTCTCAAT CCGTGAAGGT GGTAAACTG TAGGTCATGG T 891

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 909 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Wolinella succinogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

00989643 "12004
AACATGATTA CAGGTGCTGC TCAAATGGAT GGC GCGATT C TTGTTGTTTC TCGGCGGAT 60
GGCCCCATGC CCCAAACTAG GGAGCACATT CTTCTTTCTC GACAAGTAGG CGTTCCTTAC 120
ATCGTGGTTT TCTTGAACAA AGAAGATATG GTTGATGACG CTGAGCTTCT TGAGCTTGTT 180
GAAATGGAAG TTAGAGAACT TCTTAGCAAC TACGACTTCC CTGGAGATGA CACTCCTATC 240
GTTGCAGGTT CCGCTCTTAA AGCTCTTGAA GAGGCTAACG ACCAGGAAAA TGTTGGCGAG 300
TGGGGCGAGA AAGTATTGAA GCTTATGGCT GAGGTTGACC GATATATTCC TACGCCTGAG 360
CGAGATGTGG ATAAGCCTTT CTTATGCCT GTTGAAGACG TATTCTCCAT CGCGGGTCGT 420
GGAACCGTTG TGACAGGAAG AATTGAAAGA GCGTGTTA AAGTCGGTGA CGAAGTAGAA 480
ATCGTTGGTA TCCGAAACAC ACAAAAAACA ACCGTAACG GCGTTGAGAT GTTCCGAAAA 540
GAGCTCGACA AGGGTGAGGC GGGTGACAAC GTTGGTGTTT TTTTGAGAGG CACCAAGAAA 600
GAAGATGTTG AGAGAGGTAT GGTCTTTGT AAAATAGGTT CTATCACTCC TCACACTAAC 660
TTTGAAGGTG AAGTTTACGT TCTTTCCAAA GAGGAAGGCG GACGACACAC TCCATTCTTC 720
AATGGATACC GACCTCAGTT CTATGTTAGA ACTACAGACG TTACCGGTTT TATCTCTCTT 780
CCTGAGGGCG TAGAGATGGT TATGCCTGGT GACAACGTTA AGATCAATGT TGAGCTTATC 840
GCTCCTGTAG CCCTCGAAGA GGGAACACGA TTCGCGATCC GTGAAGGTGG TCGAACCGTT 900
GGTGCGGGT 909

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:18
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

TARTCNGTRA ANGCYTCNAC RCACAT

26

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

TCTTTAGCAG AACAGGATGA A

21

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

GAATAATTCC ATATCCTCCG

20

0021496860